GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        32.4
30.4
30.4
30.4
     2299222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.Seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.Seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.Seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
    100.0
70.4
70.4
40.0
37.5
37.5
37.0
37.0
36.8
36.8
36.8
36.8
36.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                  Length
   392
415
549
2686
3380
5617
648
653
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658
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    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (without alignments)
6329.459 Million cell updates/sec
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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1786, Ap
Sequence 9137, Ap
Sequence 2178, Ap
Sequence 49, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 51, Appli
Sequence 66, Appl
Sequence 66, Appl
Sequence 68, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 52, Appli
Sequence 52, Appli
Sequence 52, Appli
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28.6 27.6 27.6 27.6 27.6 27.6 27.6 27.6 27	2222229 22229 239 244 365 444 365
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6158 1720 5720 684973 2740 3913 1155074 2259 2256 3226 3236 3236 3236 3236 3236 3236	823 88191 1619 821 1176 1574 886 6158
100 100 100 100 100 100 100 100 100 100	10 9 9 10 10
US-09-954-456-762 US-09-813-242-7615 US-09-813-79-56 US-09-23-3-79-56 US-09-23-876-4300 US-10-026-188-6 US-09-965-188-6 US-09-765-231A-49' US-09-962-436-308 US-09-962-436-725 US-10-044-090-448 US-09-924-340-57 US-10-033-297-3 US-10-033-297-3 US-10-031-806-3 US-10-0777-430A-9 US-09-777-430A-9	US-09-923-779-28 US-09-799-799-3 US-09-764-868-400 US-09-729-658B-14 US-09-729-658B-1 US-09-729-658B-1 US-09-923-779-6
761 761 761 761 761 761 761 761 761 761	Sequence 28, Appl Sequence 3, Appli Sequence 400, Appl Sequence 7, Appli Sequence 14, Appli Sequence 1, Appli Sequence 6, Appli

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### ALIGNMENTS

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RESULT 2
US-09-997-610-5
; Sequence 5, Application US/09997610
; Patent No. US20020156244A1
                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (2)...(1381) US-09-997-610-1
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                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09997610 Patent No. US20020156244A1
                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 81; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FOX, Brian
APPLICANT: HOILOWAY, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/97,610 CURRENT FILING DATE: 2001-11-29 PRIOR APPLICATION NUMBER: US 60/253,924 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                          1381
                                                                                                                                                                                                                                         Score 81; DB 9;
Pred. No. 7.1e-18;
; Mismatches 0;
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GENERAL INFORMATION:

TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN TITLE OF INVENTION: ZACRP13

FILE REFERENCE: 00-96

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NAME/KEY: misc_feature
LOCATION: (1)...(1377)
OTHER INFORMATION: n = A,T,C or
US-09-997-610-3
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; LOCATION: (1)...(1731)
US-09-997-610-5
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LENGTH: 1731
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/253,924 PRIOR FILING DATE: 2000-11-29 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/253,924 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/997,610 CURRENT FILING DATE: 2001-11-29
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                          NAME/KEY: variation
LOCATION: (1)...(1377)
OTHER INFORMATION: Each n is independently A,
                                                                                                                                                                                                                                             OTHER INFORMATION: Degenerate OTHER INFORMATION: of SEQ ID 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                            LENGTH: 1377
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 55
                              1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60
 GGNCCNCCNGCNCAYCCNMGNCCNCCNGARGARGTNGGNCCNCCNGGNGCNCCNGGNYTN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
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                                                                Conservative
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                                                                              70.4%;
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                                                           Score 57; DB 9; LC
Pred. No. 6.7e-10;
Prematches 20;
                                                                                                                                                                                                                                               polynucleotide encoding a polypeptide NO:2
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Pred. No. 7.6e-18;
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                                                                                              Length 1377;
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                                                                Indels
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80

1 GGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60

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; NAME/KEY: misc_feature
: LCCATION: (1)...(1731)
: OTHER INFORMATION: n = A,T,C or G
US-09-997-610-7
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                                                                              US-09-960-352-1786
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                                                                                      SEQ ID NO 1786
LENGTH: 392
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 08-LIB34-023-Q1-E1-B7
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Best Local Similarity
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                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1786, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Matches
                                                                                                                                                                                                                   APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10208)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 00-96
                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Degenerate polynucleotide sequence of zacrp13/zhp1 OTHER INFORMATION: of SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 GGNCCNCCNGCNCAYCCNMGNCCNCCNGARGARGTNGGNCCNCCNGGNGCNCCNGGNYTN 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 CCNCARTAYACNGGNGARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCACAATATACAGGAGAAATA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCACAATATACAGGAGAAATA 81
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1 Similarity 48; Conserv
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  Conservative
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64.28;
                   40.0%;
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Pred. No. 7.2e-10;
                   Score 32.4; DB Pred. No. 0.069;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1731;
                                      Length
                                          392;
  0;
  Gaps
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                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: 480, 498, 523, 539
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB34-018-Q1-E1-B12
US-09-960-352-9137
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                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Warren, V
                                        Matches
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49, Application US/09923779 Patent No. US20020076721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 415
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                    LENGTH: 549
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                                                       Local Similarity
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GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60
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48; Conserv
                                      Conservative
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                                                     37.5%;
                                                                                                                                                                                                                                                                     Windows Version 4.0
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                                                   Score 30.4; DB Pred. No. 0.35;
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Pred. No. 0.07;
                                      Mismatches
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                                                                    Length
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US-09-880-107-2178
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GENERAL INFORMATION:
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 48
LENGTH: 2686
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Best Local
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
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                                                                                                                                        LOCATION: (2505)
OTHER INFORMATION: n equals a.t.g,
                                                                                                                                                                         FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                  OTHER INFORMATION:
NAME/KEY: SITE
                                                   NAME/KEY: SITE
LOCATION: (2644)
                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  TYPE: DNA
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les 40; Conserva
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Scherf, Uwe
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                                 equals a,t,g,
                                                                                    equals a,t,g,
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Pred. No. 0.6;
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548 US-09-880-107-2178
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                              670 GGCCCTCCAGGACCCAAGGGCCCCCAAAGGAGTGGGCCCCCCCGGACCACCACCAGG 725
                                                                                                                                                                                                                                                                                                                                                                                       1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGG 56
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                                                                                                                         and Antibodies
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Query Match
Best Local Similarity
Watches 48; Conserva
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; ORGANISM: Human
US-09-799-799-1
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; OTHER INFORMATION: n = A,T,C or G US-09-923-779-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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Best Local Similarity
                                                                                                                          SEQ ID NO 47
LENGTH: 561
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TITLE OF INVENTION: NUC:
TITLE OF INVENTION: PRO'
FILE REFERENCE: CL001157
                                                                                                                                                                                                                                                                                         APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
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CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC FILE REFERENCE: 210121.553
                        PEATURE:
NAME/KEY: misc_feature
LOCATION: 544, 550
                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                    ORGANISM: Homo sapiens
                                                                                                           TYPE: DNA
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61.5%;
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61.5%;
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Pred. No. 0.82;
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CANCER
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Query Match
Best Local Similarity
Watches 49; Conserve
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, NAME/KEY: misc_feature
; LOCATION: 581, 605
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-51
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                                                                                            CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 617
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                                                                                                                                                                                                                                                                                                                                         Sequence 66, Application US/09923779 Patent No. US20020076721A1
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                                                                                                                                                                                           APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANC
FILE REFERENCE: 210121.553
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APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
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CURRENT FILING DATE: 2001-08-06
                                                         LENGTH: 64
TYPE: DNA
                                     ORGANISM: Homo sapiens
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                      FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 GGATCTCCAGGATACCAAGGACCCCCTGGTGAACCTGGGCAAGCTGGTCCTTCAGGCCCT 465
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; LOCATION: 642, 646 ; OTHER INFORMATION: n = A,T,C US-09-923-779-66

or

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Patent No. US20020076721A1

GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.53
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 53
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 517, 579, 581, 603, 649
OTHER INFORMATION: n = A,T,C or G
US-09-923-779-53
      APPLICANT: Pyle, Ruth A.

APPLICANT: Xu, Jiangchun

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.553

CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 155

SOSTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 68

LENGTH: 655
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; Sequence 68, Application US/09923779
; Patent No. US20020076721A1
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; NAME/KEY: misc_feature
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COTHER IMFORMATION: n = A,T,C or
US-09-923-779-68
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Search completed: February 19, 2003, 23:02:28 Job time: 11.518 secs
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                              466 CCAGGACCTCCTGGTGCTATA 486
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                                                                                             61 CCACAATATACAGGAGAAATA 81
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

MODEL-frame+\_p2n.model -DEV=xlh
-O-/Cgn2\_1/USPTO\_Spool/US09997610/runat\_10022003\_160823\_23843/app\_query.fasta\_1.1635
-O-/Cgn2\_1/USPTO\_Spool/US09997610/runat\_10022003\_160823\_23843/app\_query.fasta\_1.1635
-DB-EST -OPMY-fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END--1 -MATRIX=blosum62 -TRANNS-human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE-pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER-US0997610\_eCGN\_1\_1\_1871\_erunat\_10022003\_160823\_23843 -NCPU=6 -ICPU=3
-NO\_XUPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES-0 -WAIT -LONGLOG -DEV\_TIMEOUT=120
-WARN\_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7 Minimum DB Maximum DB OM protein - nucleic search, using frame\_plus\_p2n model Scoring table: Title: Perfect score: Run on: Database : Total number of hits satisfying chosen Sequence: Post-processing: Minimum Match 0% Maximum Match 10 seq length: 0 seq length: 2000000000 -YGAPEXT=0.5 -DELOP=6 -DELEXT= Xgapop 10.0 , X Ygapop 10.0 , X Fgapop 6.0 , I Delop 6.0 , I February 19, BLOSUM62 US-09-997-610-2\_COPY\_1\_149 790 16154066 seqs, 8097743376 residues IVVIPVLITAVIEHVEVAGP...... gb\_est1: \*
gb\_est2: \*
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gb\_est3: \* em\_estov:\*
em\_estpl:\* em\_estom:\*
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2084.671 Million cell updates/sec KEEISKQQSIQEVTWVLLKA 149 32308132

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.		Query Match	Length	DВ	ID	Description
υμ	J	» ·	199	14	BM967732	67732 LM2
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9 1		9 :	9	Ė	K01874	K018742 Mus
10	15	9.	66	14	41995	419957 faa12c
11	55.	9.	9	9	43093	093 AV243
c 12	54.	9.	8	14	1938	193813 UI-R-CN
13	54.	9.	N	9	73154	3154 ve40g07.r
14	52.	9.	6	10	W98855	W988554 ug08h07
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17	52.	9 4	ο u	12	272	G872725 6027938
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20	0	9	0	9	A49309	93090 v171g11
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## ALIGNMENTS

REFERENCE AUTHORS RESULT 1 BM967732 LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION EST. BM967732
499 bp mRNA lines LM24+HW-0134 Bos taurus LM-24-HW cDNA library Bos LM-24-HW-011-34 (5'), mRNA sequence. COW. LM-24-HW-011-34 BM967732 1 (bases 1 to 499) Yoon, D.H., Jang, Y.S., Bovidae; Bovinae; Bos. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bos taurus вм967732.1 GI:19561919 Kim, T.H., Park, E.W., Lee, H.K., Chung, E.R., linear ar EST Euteleostomi; cora; Bovoidea; cDNA clone

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                                                                                                                   CTGCAAGGTGACTGTT 489
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Contact: Dr. Du.Hak Yoon
National Livestock Research Institute, RDA
564 Omockchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhyoon@rda.go.kr
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Seq primer: CAGGAAACAGCTATGAC
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EcoRI; Site_2: Xho I"
1 139 c 131 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="longissimus dorsi"
/cell_type="myocyte"
/dev_stage="24 months old"
/lab_host="XL1-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Bos taurus LM-24-HW cDNA library"
/sex="six males mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
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             GI:10171268
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                                       526 bp mRNA linear Bos taurus cDNA 5', mRNA sequence
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                                    241 CCAGGACTAACAGGGAGACCTGGGCTTCCTGGACTGGTTGAGAAG-----
                                                                                                                                                                                                                                                                                                                                                                              181 GGACCTCCGGGACTCAGTGGTCTTCCAGGGCCACCTGGTTATACAGGACCCATAGGTATG
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                        MetGlyValPheAlaCysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeu 112
ACTGGTGTTCAGCTGCAGCGTCCCTGGTGTACCACTTTGGCTTTGACATTGAGTTG
                                                                                          TCCCAGCCCATTGTCTTCCAGGAAGTTCTGTACAACCATCAGGGCCACTTCGACCCCGCC
                                                                                                                                   PheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAla 92
                                                                                                                                                                                       TGCCCACCCCTGCCTCAGTCTGCCTTTTCCGTCAAGCTGAGTGGGCCTTTCCCCAGGACCC
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A..., Smith, T.P.L., Grosse, W.M., Freking, B.A., Fahrenkrug, S.C., Benneti Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Benneti Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Chitko-McKown, G.I.., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, G.I.., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, J. a horrton. G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. a horrton. G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. a horrton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGACG
BACKWARD: TOW: G COLUMN: 14
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

137 c 153 g 130 t
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/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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Library made from pooled tissue from test
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CysProAspIleGluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuPro
                                                                                                                                                                      GGACCTCCGGGACTCAGTGGTCTTCCAGGGCCACCTGGTTATACAGGACCCATAGGTATG
                                                      CCAGGACTAACAGGGAGACCTGGGCTTCCTGGACTGGTTGAGAAG---
                                                                                                                ProGlyLeu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USTA: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="MARC 2BOV"
/tissue_type="pooled"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; S
/note="Vector: pCMV SPORT
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/db_xref="taxon:9913"
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Contact: Tadasu Shin-i
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BJ068972 HSD Mochii normalized Xenopus tailbud li
laevis cDNA clone XL051f08 5', mRNA sequence.
BJ068972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
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1 (bases 1 to 663)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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81-559-81-6856
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/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
/were oligo-dT primed and darectionally cloned. Staging
according to Nieuwkoop and Faber: Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
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160 c 164 g 160
                                                                                                                                                                                                                                                                                                                                                                                             library"
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/db_xref="taxon:8355"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Saurin,W. and Weissenbach,J. Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                   Bernot, A. and Weissenbach, J.
Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1092)
Crollius, H.R., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin
                                                                                                                                                                                              Genoscope.
Direct Sub
                                                                                                                             Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis scale clone-end sequencing project ake a look at
                                                                                                        genome. For more information, please thttp://www.genoscope.cns.fr/Tetraodon
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/db_xref="taxxon:99883"
/clone="011D22"
/clone_lib="A"
                                                                                           Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                                                        Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855
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Kohara,Y., Shin-i,T., Kimura,T., Ne
Medaka EST Project in Takeda's lab
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Contact: Tadasu Shin-i
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301 c 308 g 245 t 14 others
                                                               tshini@genes.nig.ac.jp.
Location/Qualifiers
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32.06%
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/db_xref="taxon:8090"
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                          /strain="d-rR"
                                        /organism="Oryzias latipes"
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/clone\_lib="MF01FSA cDNA"

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Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                    Establishment of a high throughput EST sequencing poly(A) tail-removed cDNA libraries and determinate
                                                                                                                                                          Takasuga, A.,
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                 Bos taurus
05 5′, mRNA
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/tissue_type="whole embryo"
/dev_stage="fry stage 40"
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l (bases 1 to 689)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Saski,D., Shidata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

On Jul 11, 2000 this sequence version replaced gi:9025815.
                                                                                                                                                                                                                                                                                                                               BB318780
BB318780
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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BB318780
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This clone was obtained from a
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mina Mus musculus cDNA clone B230377C02 3', mRN
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/dev_stage="fetus"
/lah hore-"-""
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/note-"Vector: pzLl; Site_1:
was deleted from a Not1 site"
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/clone="E1CA005A05"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Encyclopedia Project of Genome Exploration Research Group in
Genomic Sciences Center and Genome Science Laboratory in RIKE
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with juman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site_1: SalI; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male'
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK018742 2462 bp mRNA linear HTC Mus musculus adult male kidney cDNA, RIKEN full-length e library, clone:0610011L15:procollagen, type VIII, alpha
                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (strain:C57BL/6J) adult male kidney clone_lib:RIKEN full-length enriched mouse cDNA l
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18 AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohar Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Hofmann,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              cleaved with XhoI and SstI. Cloning sites, 5' end: SstI;
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                                              /strain="C57BL/6J"
/db_xref="FANTOM_DB:0610011L15"
/db_xref="MGD:MGI:1912859"
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GGCAACGTATGGGTT 2227
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                                       ValAsnIleTrpLeu 121
                                                                                     TGTGAAGTCCCGGGTGTCTACTACTTTGCTTATCATGTT--
                                                                                                                               CysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeuHisHisCysLys--- 116
                                                                                                                                                                           TTTGACAAGCTGCTCTACAACGGCAGACAGAACTACAATCCGCAGACAGGCATCTTCACC 2161
                                                                                                                                                                                                                  PheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPheAla 97
                                                                                                                                                                                                                                                              ATGCCTGCGTTTACTGCCGAGCTGACTGTACCTTTCCCACCGGTGGGGGCCCCCAGTGAAG 2101
                                                                                                                                                                                                                                                                                                        ArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLysProIleIle 77
                                                                                                                                                                                                                                                                                                                                                      GTGAAACCTCCGCATGCCTATGCGGGCAAAAAAGGGCAAACACGGAGGGCCAGCCTATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ProGlnTyrThrGlyGlu-----
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/translation="MAVPPRPLQLLGILFIISLNSVRLIQAGAYYGIKPLPPQIPPQI
PPQIPQYQPLGQQVPHMPLGKDGLSMGKEMPHMQYGKEYPHLPQYMKEIPPVPRMGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQMPSEQAAGLYAGQYVHSSFSGYL
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PGMPGMPGKPGAMGMPGAKGEIGPKGEIGPMGIPGPQGPPGPHGLPGIGKPGGPGLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB31383.1"
/db_xref="GI:12858613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="data source:MGD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Col8a1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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	ProGlyAlaProGlyLeuProGlnTyrThrGlyGluIle		ОУ
o 32     269	GlyProProAlaHisProArgProProGluGluValGlyPro	19 G 210 G	Qу
	610-2_COPY_1_149 (1-149) x BQ419957 (1-662)	09-997-	us-
	Alignment Scores: 1.52e-06 Length: 662 Score: 157.00 Matches: 43 Scores: 20 Percent Similarity: 43.458 Conservative: 20 Best Local Similarity: 29.668 Mismatches: 46 Query Match: 19.878 Indels: 36 DB: 14. Gaps: 5	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Alignm Pred. Score: Percen Best I Query DB:
hoI; 1st followed apter (5' cloned xpress obtain	/db_xref="taxon:7955" /clone="5909744" /clone="5909744" /clone="5909744" /clone="16" /sex="mixed male and female" /tissue_type="3 day fin regenerates" /lab_host="E. coli XLOLRe" /note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; listrand cDNA primed with (GA)LOACTAGTOCGAG(T)18, follooby second strand synthesis, and ligated to 5 adapter )-aattcggcacgag- 3, 3'-gccgtgctc-5', cDNA was cloned directionally (EcoRI/XhoI) into Stratagene Zap express lambda phage arms. Mass invivo excision done to obtainserts in pBK-CMV phagemid."  161 a 192 c 152 g 157 t	BASE COUNT	BAS
	<pre>Seq primer: T3 ET from Amersham High quality sequence stop: 468. Location/Qualifiers 1662 /organism="Danio rerio"</pre>	FEATURES Source	FEA
ad by: anome Louis, act: Alabama com) and bress:	Fax: 314 286 1810  Email: zbrafish@watson.wustl.edu  Email: zbrafish@watson.wustl.edu  cDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:  Matthew Clark. DNA Sequencing by: Washington University Genome  Sequencing Center Clone distribution: Genome Systems, St. Louis,  Missouri (web address: www.genomesystems.com) (email contact:  info@genomesystems.com) and Research Genetics, Huntsville, Alabama  (web address: www.resgen.com) (email contact: info@resgen.com) and  RessourcentZentrumPrimarDatenbank, Berlin, Germany (web address:  www.rzpd.de)		
USA	and witsou, K. WashU Zebrafish EST Project 1998 Unpublished (1998) Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, University School of Medicine	TITLE JOURNAL COMMENT	COM
rra,M., Eddy .T., Underwood rson,B., , Ritter,E., waterston,R.	; Cyprinidae; Danio.  1 (bases 1 to 662)  1 (bases 1 to 662)  1 (bases 1, Li, F., Marra, M., Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Un, S., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., K., Steptoe, M., Theising, B., Harvey, N., Schurk, R., Ritte Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waters Swaller, M., McCann, R., Waters Swaller, T., Gibbons, M., McCann, R., Waters Swaller, M.,	REFERENCE AUTHORS	REFI
 .niformes	R1 repetitive element ;, mRNA seque 158 150chordata; Craniata; Vertebrata; Eutervali: Teleostei: Ostariophysi; (	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	ACCI VERS KEYV SOUI
23-MAY-2002 CDNA clone TYPE X	BQ419957 662 bp mRNA linear EST 23 faa12c05.y1 zebrafish fin day3 regeneration Danio rerio cC 5909744 5' similar to TR:Q9Z1K4 Q9Z1K4 COLLAGEN ALPHA 1 TY	ITION	LOCUS

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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Inpublished (2001)

On Nov 4, 1999 this sequence version replaced gi:6230520.

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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,K., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagama,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV243093 RIKEN full-length enriched, O day neonate musculus cDNA clone 4831416G24 3', mRNA sequence.

AV243093 _______
                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninoi, P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninoi, P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA librarias for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
yeagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura
Ns., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa;
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugrand
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
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              Carninci, P., Sugahara
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encyclopedia: real-time sequence

construction of a

Y. and Hayashizaki,Y.

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US-09-997-610-2_COPY_1_149 (1-149) x AV243093 (1-695)
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                                                                                                                                                                   245 GTGAAACCTCCGCATGCCTATGCGGGCAAAAAGGGCCAAACACGGAGGGCCAGCCTATGAG
                                                                                                                                                                                                                                                             185 ATGCCTACACCATCACCCCAGGGAGAGTATCTGCCAGATATGGGAACTAGGAATTGATGGG
                                                                                                                                                                                                                                                                                                                                                       125 GGCCAGCCTGGCCTTCCTGGACCCCCAGGTCTTCCAGGACCCCCAGGCCTTCCAGCTGTG 184
78 PheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPheAla 97
                                                                                                                                                                                                                                                                                                                                                                                                   19 GlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGlyLeu
                                                                                                                                                                                                                                                                                                           39 -----ProGlnTyrThrGlyGlu------
                                                                                                                  ArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLysProIleIle 77
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Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please.visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Ai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with numan Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D
                                                                                                                                                                                                              --------IleSerGluMetThrLysCysProCysProAspIleGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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/clone="4831416G24"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strand CDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oilgo-dT track served to identify it as a clone from the normalized fundus library cDNA Library Preparation: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first
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Fax: 319 335 9565
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
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bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CN1 library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plantid DNA template preparation) comprising: a) a pool of about 34,000 clones from the Rat Unique Set corresponding to plates R-5-AA-NN excluding plates R-5-AM and NN This pool represented Ana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1
polylinker; sa subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
places of the property of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UI-R-CN1-clw-p-16-0-UI"
/clone_lib="UI-R-CN1"
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Rodentia;
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                                                                                                                                                               The WashU-HHMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                           i (bases 1 to 921) marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 499.
                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                       Email: mouseest@watson.wustl.edu
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                   REFERENCE
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468 bp mRNA linear EST 02-JUN-2000 ug08h07.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone lMAGE:1531069 5' similar to gb:037222 Mus musculus 30kDa adipocyte complement-related protein Acrp30 (MOUSE); mRNA sequence.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 468)
                                                                                                                                    AW988554
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                                                                                   house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
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/db_xref="taxon:10090"
/clone="IMAGE:820668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary gland"
/dev_stage="4 weeks"
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                                                                                                                                                                                                           ACCTACGACCAGTATCAGGAAAAGAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTC 402
                                                                                                                                                                                                                                                    AsnLysGluGluIleSerLysGlnGlnSerIleGlnGluValThrTrpValLeuLeu 147
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                                                               BE625509 552 bp mRNA linear EST 24-AUG-2000 uu19e06.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3372418 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
                   complement-related protein Acrp30 (MOUSE);, mRNA sequence.
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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GI:9905925
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KEYWORDS
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                                                                                                         GluLeuHis-----HisCysLysValAsnIleTrpLeuMetArgLysGlnIleLeuAla 128
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                                    AsnLysGluGluIleSerLysGlnGlnSerIleGlnGluValThrTrpValLeuLeu 147
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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Search completed: February 19, 2003, 19:35:55

Job time : 1161.56 secs

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Title:
Perfect score:
Sequence:
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-MODEL-framet_p2n.model -DEV=xlh

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-Q-/Ggn2_1/USPT0_Spool/US09997610/runat_10022003_160823_23819/app_query.fasta_1.1635

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXXIEN=2000000000

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-NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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5 Mus 6 Mus 7 Mus 8 Mus 8 Mus 8 Homo 9 Seque 9 Seque 10 Homo 11 Mus 11 Mus 12 Homo 12 Homo 13 Homo 14 Macaa 15 Homo 17 Mus 17 Mus 17 Mus 18 Homo		Description  Z82198 Human DNA s AF01777 Drosophil AC013980 Drosophil AC021494 Drosophil AC011251 Drosophil AE003568 Drosophil AE003568 Drosophil AC024805 Caenorhab AC066799 Caenorhab AX146422 Sequence AX146424 Sequence AX146423 Xenopus 1

ALIGNMENTS

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP1-302D9 The end of clone CTA-282F2 is at 69682 in this sequence. The t end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP1-302D9 is from the library RPCI-1 constructed at the Park Cancer Institute by the group of Pieter de Jong. For details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Dec 13, 1999 this sequence version replaced gi:3164067. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feature key.
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              /note="AluSq repeat: 3323. .3343
                                                     2684.
                                                                                                                            1687
                                                                                                                                                             1450.
                                                                                                                                                                                                                                  783
                                                                                                                                                                                                                                                                   /note="AluSx repeat: 572. .759
                                                                                                                                                                                                                                                                                                        246.
                                                                                                                                                                                                                                                                                                                                        /clone="RP1-302D9"
/clone_lib="RPCI-1'
188. .245
                                                                                                                                                                                             /note="MER5A repeat: 1033. .1336
/note="MLT1E repeat: matches 116. .136 of consensus"
                                                                                                                                                             /note="AluSp repeat: matches 1.
1450. .1583
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                    'note="AluSc repeat:
                                                                                                       note="I
                                                                                                                                           'note="MIR repeat: matches 24.
                                                                                                                                                                                                                                                 /note="MER3 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                       note="MER3 repeat: matches 144. .209 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="22"
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                                                                                         .2660
                                                                                                                                                                                                                                                                                                                                                          _lib="RPCI-1"
                                                                                                      repeat: matches
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                                                                    matches 3.
                                                                                                                                                                                                             matches 26.
                                                                                                                                                                                                                                                                                    matches 1.
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                                                                                                       2593.
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                                                                    .309 of consensus"
                                                                                                                                                                              . 299
                                                                                                                                                                                                                                                                                    .312
                                 .300 of consensus"
                                                                                                       .2661 of
                                                                                                                                                                                                               .187 of consensus"
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                                                                                                    /note="MIR
14061. .143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 1.6988. 7036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6686.
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7775. .8060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MADE1 repeat: matches 23.
7482. 7754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MLT1E repeat: matches 136. .359 3929. .4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 1, .309 of consensus" 3653, .3928
                                                                                                                                         /note="MIR repeat: matches 77.
13945. .14060
                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 20.
12174. .12445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(10249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10204.
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                               /note="MIR repeat: matches 141.
14589...14679
                                                                                                                                                                                                                                                                                                                       13017
                                                                                                                                                                                                                                                                                                                                                          12444
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: 11838...11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(10179.
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/note="FAM r
                                                                      14368.
                                                                                                                                                                                           note="MIR repeat: matches 76.
                                                                                                                                                                                                                 13699.
                                                                                                                                                                                                                                                    13398
                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 174.
                                                                                                                                                                                                                                                                                      /note="match:
|3331. .13397
                                                                                                                                                                                                                                                                                        13331
                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat:
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                                                                                                                                                                                                                                  'note="AluSp repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                          . 241
                                                                                                                                                                                                                                                                                                                                                                                                              .137 of consensus"
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                                                                                       .301
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                .262 of
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Em: AQ553482

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                                                                                                                                                                                                                        Best Local Similarity:
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                 ProAlaHisProArgProProGluGluValGlyProProGlyAlaProGly 37
                                                                                        IleValValIleProValLeuIleThrAlaValIleGluHisValGluValAlaGlyPro
CCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGT
                                                                     ATAGTGGTCATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCT
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/note="MiTIB repeat: matches 178 . .390 of consensus" 16546 . .16854
/note="AluX repeat: matches 1 . .300 of consensus" 1832
                                                                                                                                                                                                                                                                                                                                                                   consensus"
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18324. .18392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1B repeat: matches 119. .178 of consensus"
15728. .16027
                                                                                                                                                                                                                                                                                                                                  /note="MER66-internal repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER66-internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER66-internal repeat: matches 4919. .4993
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                                                                                                                                                                                                                                                                                                                                                                                        /note="MER66-internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSg1 repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="77
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AF01777.1 GI:3004652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 66669)
Miklos,G.L., Yamamoto,M., Burns,R.G. and Maleszka,R.
An essential cell division gene of Drosophila, absent from
Saccharomyces, encodes an unusual protein with tubulin-like and
myosin-like peptide motifs
Proc. Natl. Acad. Sci. U.S.A. 94 (10), 5189-5194 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biological Sciences, The Australian National University,
Creek Rd., Canberra, ACT 0200, Australia
On or before Apr 2, 1998 this sequence version replaced g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maleszka,R., de Couet,H.G. and Miklos,G.L.
Data transferability from model organisms to human beings: insights from the functional genomics of the flightless region of Drosophila Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3731-3736 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gi:1052878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall,D. and Maleszka,R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular and mutational analysis of a gelsolin-family member encoded by the flightless I gene of Drosophila melanogaster Genetics 141 (3), 1049-1059 (1995)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 66669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-AUG-1997) Visual Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miklos, G.L.G., Kasprzak, A., Mason, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl.
97289742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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                                            Translation="MGDYHEFTDQYKVPVIAKLLHALPHYNITFHKINSTFRPNDEIY
LESLGILGSVPAALLIVSLLGLLFYLMTRCCDRKPRPAHSITSLKVALSIVTVMCCAA
IGLGLYGNDDLHNGLLEVLTAGRKVDNLVTTIRNQTHILENTLTNRIRPQLVELADIF
                                                                                                                                                                                                 complement(join(1767. 3917. .4680,4745. .52
                                                                                                                                                                                                                                                                        complement(join(1639. .2707,2789. .2800,3622. .37) 3917. .4680,4745. .5230,5525. .5809,7521. .7694))
                            DQPVSNQTALSKLFVSLNIVQGNVTLATNAASDIRRPLMGISMTHFLTRGDQWELIRW
                                                                                                   /product="tweety"
/protein_id="AAC28400.1"
/db_xref="GI:3004653"
                                                                                                                                                                                                                                                                                                             /gene="tty"
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                                                                                                                                                                              /gene="tty
                                                                                                                                                                                                                                    /product="tweety"
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                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7227"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/strain="CantonS"
                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                 .5230,5525.
                                                                                                                                                                                                                 2707,2789
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                                                                                                                                                                                                   .5662))
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/db_xref="GI:3004661"
/translation="MPDAEQLPDGWEKRTSRSTGMSYYLNMYTKESOWDQPTEPAKKT
/translation="MPDAEQLPDGWEKRTSRSTGMSYYLNMYTKESOWDQPTEPAKKT
GGGSAGGGDAPDEVHCLHLLVKHKGSRRPSSWREANLTRTKEEAQLLLEVYRNKIVQQ
EATFDELARSYSDCSSAKRGGDLGKFGRQQMQAAFEDAAFKLNVNQLSGIVDSDSGLH
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QGETRTDLAALFWBRQSAMPLABABQLEEEWNVDLEMMEAFVLENKKFVRLDEEEELGR
FYTGECYVFLCRYCIFLEEDENGSEDGGANPAADVSKSSANMOPEDBIOCVVYFWOGRN
AGNMGWLTFTFTLQKKFKAMFGEELEVVRIFQOQENLKFMSHFKRKFIIHTGKRKDKA
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AYGATIHLEPVAPAITSLDPRHAFVLDLGTHIYIWMGERSKNTLNSKARLMAEKISKT
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KPSILNCPLPEIPKDAEQPKVESIYEQRQQAHHQNYSK"
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GPQIPAHQHPPSLHQQQQQPPPPSQQQQQLHQLKSPQQHQQQLQQHQQQQQQQQQHHQQQ
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LLGLVLMLLASFLAAILLTIMWWDSHTWIYIRKRNDYAQVDEPSYISHAPQNHQQM
MNAARTLFRNHWGHFSPBYJGGSHTLOHPSKRQQHEMMAHAHIQQNMRAWGTHTLGRL
PSHNHSPTHMTGPNNAAAVAAAANAANMPPTTQAAQQQQQQQQQQQQQQQQQQQCGGP
                                                                                                                                                                                                        complement(join(15308. .15493,15707.
16752. .17454,18055. .18500))
                                                                                                                                                                                                                                                                                                                                                complement(join(15247. .15493,15707.
16752. .17454,18055. .18587))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERKNKCEIQLERQGEESAEFWQGLGMTSEEADAAEPPKEHVPEDYQPVQPRLYQVQLG
MGYLELPQVELPEQKLCHTLLNSKHYYILDCYTDLFVWFGKKSTRLVRAAAVKLSREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNKIEEVVHGKFYEGDCYIVLKTKFDDLGLLDWEIFFWIGNEATLDKRACAAIHAVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDKDNEAGAVPEDGKPESLKPKRWDESLEKPQLDYSKFFEKDDGQLPGLTIWEIENFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFSLQTQLRLAGAAVPPSMPSSATPKDSTARKIRLRRGPRSEGDQDAAKVLKGMKDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGALKQLNLSCNRLITLPDAIHLLEGLDQLDLRNNPELVMPPKPSEASKATSLEFYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANLCELDLSHNSLPKLPDCYYNVYTLYRLNLSDNELTELTAGVELWQRLESLNLSRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLPPQTRRLINLKTLDLSHNPLELFQLRQLPSLQSLEVLKMSGTQRTLLNFPTSIDSL
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/protein_id="AAC28407.1"
/db_xref="GI:3004660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5809. .7521)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(15247. .18587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKLAYKSAQVYIQHMRIKQPERPRKLFLTMKNKESRRFTKCFHGWSAFKVYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYMNYTRLFRCSNERGYYTVAEKCADFCQDDLADDDIMILDNGEHVFLWMGPRCSEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVWIGSKACNEEAKLVQDIAEQMFNSPWVSLQILNEGDEPENFFWVALGGRKPYDTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTAKGKSPVEFFHLRSNGGALTTRLIQINPDAVHLNSAFCYILHVPFETEDDSQSGIV
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join(8652. .8705,8869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(8586. .8705,8869.
/gene="fli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IILRKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(14195. .14252,14364. .14696,15066. .15175)
/gene="dod"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(14131. .14252,14364. .14696,15066. .15603)
/gene="dod"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8586. .13783
/gene="fli"
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/protein_id="AAC28403.1"
/db_xref="GI:3004656"
                                                              'product="penguin"
                                                                                                  codon_start=1
                                                                                                                                                                           /gene="pen"
                                                                                                                                                                                                                                                                              /product="penguin"
                                                                                                                                                                                                                                                                                                                  /gene="pen"
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                                                                                                                               note="contains pumilio repeats"
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23238. ..
26004. .:
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FNLPQIKPAPQLTGIPPVAACSNSRFAIANDTFCRRKQNNNNKNQNHKVVRESGAKRK
YNFTITTLSRSAAKDAGHGQMKPLRQVVNLNLNLQQEPQQKSPANPQOLQRKTQREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="small optic
/protein_id="AAC28409.
/db_xref="GI:3004662"
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PKAKEEEPAAPLVSGIEEAGMHIVLKKILKNDGKREGTPFSQQLLQNLSSDVLKAWLG
VNRACFVLLKLVEECPALLDDCKKAIAAERSLSQILADRKTPGAKLLAAKLDIGK"
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LVTGDILNHIQGESYEKAASALAQVVVQPEWRISADAAGPQPQDKKKPHNDVEAIIAQ
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FCVQRKILKYGAPATKAKLVDSLYGHIYKLAGHSIGSGLLDSMYGSATFNQRIYMRQEF
YGDLYRKAKDSNVKTLSDTYKEATNMKASILGSVKANLDHVANKQLVDSALVHAVMLE
YLRACDEDERKLEETYVDAFAALVPHMLSTKEGSEAAVLCFYKSTPKNRRAIIKNIKEH
LLKIANHEHGHVFLISLLNALDDTKATKKAIYDHLHGDLKALMSSPYGRRVIQMLVAP
                                                                                                                                                                                                                                                                                                                                  VRVALTPADIRQESKLMENLRQLEETEALTKWQNIIQYCRDNSELFVDDSFPPAPKSL
YYNPASGAGEGNPVVQWRRPHEINCDGGAYPPWAVFRTPLPSDICQGVLGNCWLLSAL
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FDKFGGGAGKSFVKPGAGGAKKFDKSGPGGFKKFDKSGATGDKRLGGNKFRGKPQTQP
                                                                    QYPQCILAIHSSKRLLVEQISPSPHLLADAIISLTLTKGQRHEGREGMTAYYLTKGWA
                                                                                                                 VVIFRTRSPAAPEIGRLVEHSKRQVRGFVGCHKMLERDIYLLVCLAFNHWHTGIEDPH
                                                                                                                                                    CKVRSGWNEVRLQGTLQPLCSISCVLLTVLEPTEAEFTLFQEGQRNSEKSQRSQLDLC
                                                                                                                                                                                                                            DKDLIWAQLLSSRCVRFLMGASCGGGNMKVDEEEYQQKGLRPRHAYSVLDVKDIQGHR
                                                                                                                                                                                                                                                          AVLAEREDLVKEVLVTKEICGOGAYQVRLCKDGKWTTVLVDDLLPCDKRGHLVYSQAK
RKQLWVPLIEKAVAKIHGCYEALVSGRAIEGLATLTGAPCESIPLQASSLPMPSEDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSYLAPIYKDAIAADRGQDLAGSLGNRGELLAADHSHPHHHHHYLHQELEEQHQHQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQNLPANCVDCEDTRKYIKSSIELYRHFSNPALNRRWVCHACGTDNSSVTWHCLICDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="small optic lobes"
join(19361. .19602,20609. .21234,21502. .22414,22843. .23171,
23238. .24826,24899. .25405,25465. .25731,25803. .25945,
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GFSIAHRLTHRLANSRGLHDWGPPGATHCPPIENVHGLHAPRLIT"
                                         GLYVMVENRHENKWIHVKCDCQESYNVVSTRGELKTVDSVPPLQRQVIIVLTQLEGSG
                                                                                                                                                                                      LLKLRNPWGHYSWRGDWSDDSSLWTDDLRDALMPHGASEGVFWISFEDVLNYFDCIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MGTISSVLQWSCTKCNTINPTESLKCFNCGTVRKVFPQQQQQQQH/
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23238. .24826,24899. .25405,25465. .25731,25803. .25945,
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                                                                                                                Query Match:
                                                                                                                            Best Local Similarity:
                                                                                                                                                     Score:
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89.00
47.17%
39.62%
37.08%
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Indels:
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Matches:
Conservative:
 -GlyProProAlaHisProArgPro 26
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18

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REFERENCE
AUTHORS
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Query Match:
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ORIGIN
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Endontervgota; Diptera; Brachycera; Muscomorpha;
                                                                                                                       HTG.
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BACR23118,
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* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                            Drosophila melanogaster.
                                                                                                                                        AC092494
AC092494.1 GI:14701995
                                                                                                                                                                                                                                       AC092494
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Ephydroidea; Drosophilidae; Drosophila.
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Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

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McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,

Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Sequencing of Drosophila chromosome X, region 20B-20C
                                                                                            ValValIleProValLeuIleThrAlaValIleGluHisValGluValAla-----
                                                                                                                                                                                                                                    Similarity:
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Location/Qualifiers
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Berkeley Drosophila Genome Project
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Paceleb, J., Paragas, V., Park, S., Patel, S., Pfelffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C., Seguencing of Drosophila chromosome X, region 19F-20A
                                                                                                                                                                                                                                                                                                                                                                                                                          Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jun 7, 2001 this sequence version replaced gi:6087907 Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-OCT-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
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Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
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pBACe3.6)"
                                                                                                                          /clone="BACR09F10 (D1128)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                /strain="y; cn bw sp"
/db_xref="taxon:7227"
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RESULT 6
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                                                                                                                                                                                                                                                                                                     Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D.D., Merkulov, G., Milshina, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moyn, Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Barandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfelffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Champe,M., Pfelffer,B.D., Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A., Bayraktaroglu,L., Beasley,E.M., Beson,K.Y., Bayraktaroglu,L.M., Bayraktaroglu,L.M., Bayraktaroglu,L.M., Bayraktaroglu,L.M., Bayraktaroglu,L.M., Bayraktaroglu,L.M., Bayraktaroglu,L.M., 
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Klamos,I., Simpson,M., Skupskil.M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292911 bp Drosophila melanogaster genomic of 5, complete security
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1 (bases 1 to 292911)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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PUBMED
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AUTHORS
TITLE
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On Oct 9, 2000 this sequence version replaced gi:7295493
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
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                                                                                                                                                                                                  'product="CT4892"
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PSHREFILKIKKKKNIKLCKREATNDBPALKLFSWNYYENETVLMGHRGCGKSTLLKILAGL
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ELEPLTRUAGVLHVOAFVELFSEEEDVKDMHAYYTELLYWYDAHVATLTKNRHAYA
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Best Local Similarity:
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                                                                                                   Direct Submission
Submitted (24-APR-2001)
University, 4444 Forest
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Submitted (24-mAR-2000) Department of Genetics, Washington
Triversity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                       University, 6 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                 Bradshaw-Cordum, H. and DuBuque, T. The sequence of C. elegans cosmic
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                                 Submitted (22-AUG-2001) Department of Genetics, Washington
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                                                                                                     Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108,
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Submitted (07-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                 Submitted (29-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                            Submitted by:
                                                                                                                                                Louis, MO
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                                                                                                                                                                                                                                 Waterston, R.
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                   Department of Genetics, Wasl
St. Louis , MO 63110, USA,
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                      Genome Sequencing Center
                                                                                                                                            63110, USA
                                                                                Washington University
                                                                                                                                                                      St.
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NOTICE: This sequence may not be the entire insert of this clor It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions. This sequence may not be the entire insert of this clone.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

http://www.wormbase.org/db/seq/sequence?name=Y51H7C;class=Sequence For a graphical representation of this cosmid sequence and its

# NEIGHBORING COSMID INFORMATION

The 200 dq cosmid is F54D12, 200 bp overlap; the 3' overlap. cosmid is H17B01,

gene source Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Köhara (http://www.ddbj.nig.ac.ip/c-elegans/hml/CE\_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers.tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964). /note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=Y51H7C.8;c join(585. s=Sequence\* /db\_xref="taxon:6239" /chromosome="II" /organism="Caenorhabditis /strain="Bristol N2" /product="Hypothetical protein Y51H7C.8" /protein\_id="AAK39332.1" /codon\_start=1 /gene="Y51H7C.8" /gene="Y51H7C.8" /clone="Y51H7C" .6866 .630,690. .862) 8;clas

FEATURES

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TSALKNISVLADTISGRVSALDVAKTRVVGCLQLAGDMEDLGVCAEGIDDAIRSEDFE
TASQHIRFLILDQAVFQIREFKQKDATDSIRHSYEVLSSAKERLSKILKSRLTESVQ
KGDVAEMQRFIKMFPLHEPDEGLQRYSVFLNQKIDKLAEDNLAIMKAGGTDDRRNV
LYADTLFMFFEGVAEIIESNLPVLEHSYGLEKLLDFMFILQARIDEFFRRLHEEFDTR
RRLSHFNRLVDDVIHQKKAAEAVEDAPDPMEIDLENMNTSAEMYMRFVSRRIG
KNEVIRSPSGGDDDEENEEARGERHRLRKEAKEOKMDGLLNRSRYGTKMGELIGNYCL
LEHFYMLKSVQKAIKSDVKEDAGGLTSSIVDDVVFIIRKSIRRAAGSGNVDSVCATIN
NATALLDTVYHGHLRGSIQGYVTSSNFASEAFTAYQGCRVKEADAAGKEOFLLAIN
NATALLDTVYHGHLRGSIQGYVTSSNFASEAFTAYQGCRVKEADAGKEOFLLAIN
NATALLDTVHGHLRGSIQGYTSSNFASEAFTAYQGCRVKEADAGKEOFLLAIN
NATALLDTVHGHLRGSIQGYTSSNFASEAFTAYQGCRVKEADAGKEOFLLAIN
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FKSAFKNKIKQGADPYGEIDROMTMQDVEYYEAHDPFMEGFLAQIDRLLVUNGWSAREKV
DNYOTLLLLTSSEIARGIEGSLAKCOFNRYGALQLDREKGICAYLTNVAGWSAREKV
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                                                                                                                           RRLSHFNRLVDDVIHQKKAAEAVEDAPDPMEIDAIASEICMMNTSAEMYWRFVSRRIG
KNEVIRSPSGDGDDEENEEARQERHRLRKEAKEQKMDQLLNRSRVGTKMQELIGNYCL
LEHEYMLKSVQKAIKSDVKEDAGGLTRCGDKKYRKRPLKQEKIC"
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KGDVAEMQREIKMFPLIHEPDEGLQRYSVFLNQKIDKLAEDNLAIMKAGGTDDNRRNV
LYADTLFMFFEGVAEIIESNLPVLEHSYGLEKLLDFMFILQARIDEFFRRLHEEFDTR
                                                                                                                                                                                                                                                                                                                                                                         /product-"Hypothetical protein Y51H7C.6b"
/protein_id-"AAK39399.1"
/db_xref-"GI:13775531"
/db_xref-"GI:13775531"
/tanslation-"Mypothetical protein Y51H7C.6b"
/translation-"Mypothetical Research Researc
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yk400bl.3, yk400bl.5"
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http://www.wormbase.org/db/seq/sequence?name=Y51H7C.6a;cla
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/translation="mStLvQYDELLGLCDGQIQRKLNNIVLCSIGKMNEKMGLRRRVM
VQSVVEKVIKYENGGHEQMDEEQMELKF"
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/protein_id="AAK39338.1"
/db_xref="GI:13775530"
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/protein_id="AAK39333.1"
/db_xref="Gi.13775525"
/translation="MSSTKSIPADVIAKLQKFDELITKLEDAVEEVDVGVEKHFERSA
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yk560h11.5, yk118a3.3, yk118a3.5, yk560h11.3'
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.5048,5864. .6340,6802. .7129,7558. .7728)
⊾"Y51H7C.6"
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graphical representation of this gene see:
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                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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/protein_id="AAK39340.]
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5: contig of 2255 bp in length
9: gap of unknown length
6: contig of 3267 bp in length
1: contig of 17641 bp in length
5: gap of unknown length
5: gap of unknown length
8: contig of 37243 bp in length
8: contig of 37243 bp in length
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4: contig of 76169 bp in length
4: contig of 76169 bp in length
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RESULT 9
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AX146424
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Sequence 3 from Patent WO0134647.
AX146422
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Bell, M.P., Neff, T.B., Polarek, J.W. and
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/db_xref="taxon:6239"
/clone="Y51H7"
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/db_xref="taxon:9913"
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Location/Qualifiers
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Xenopus laevis
Eukaryota; Metazoa; (
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1 (bases 1 to 5358)
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/db_xref="taxon:9913"
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                                                                                                                                                                                        Direct Submission
Submitted (28-AUG-2001) Collagen Research Unit, Biocenter and Department of Medical Biochemistry, University of Oulu, P. O. 5000, Oulu 90014, Finland
Location/Qualifiers
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Bell, M.P., Neff, T.B., Polarek, J.W. and
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AX146424.1 GI:14284846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
/product="type XVIII collagen short variant"
/protein_id="AAL14257.1"
/db_xref="GI:21434789"
                                                                                                                 /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                              Direct Submission submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Project Information
Center Project Name: 0
Center clone name: RPCI-23_109A22
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DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                   Center: Joint Genome Institute Center Code: JGI
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Joint Genome Institute.
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                                                                site: http://www.jgi.doe.gov
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RPWSDPRLPEPPRVDPPPPDHHQHGNPRPLEPSPVHTHQDFNPALHLVALNAPISGSM
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COMMENT

BASE

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Consensus quality: 161724 bases at least Q40
Consensus quality: 191966 bases at least Q30
Consensus quality: 205448 bases at least Q20
Consensus quality: 205448 bases at least Q20
Estimated insert size: 220300; agarose-fp estimation
Estimated insert size: 250317; sum-of-contigs estimation
Quality coverage: 3.11 in Q20 bases; agarose-fp estimation
Quality coverage: 2.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary
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/db_xref="taxon:10090"
/chromosome="16"
/clone="RP23-109A22"
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Sequence 11 from Patent W00134647.
AX146430
AX146430.1 GI:14284849
186 bp
Sequence 30 from patent US 5773249.
AR014097
AR014097.1 GI:3971551
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Bell,M.P., Neff,T.B., Polarek,J.W. and Seeley,T.W. Animal collagens and gelatins Patent: Wo 0134647-a 11 17-MAY-2001; FIBROGEN, INC. (US)
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Sus scrofa
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E 1 (bases 1 to 186)
E 1 (bases 1 to 186)
(S Cappello, J. and Ferrari, F.A.
High molecular weight collagen-like protein polymers
AL Patent: US 5773249-A 30 30-JUN-1998;
S Location/Qualifiers
1. 186
1. 186
27 t
                                                   19 GlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGlyLeu 38
  97
                  39 ProGlnTyrThrGlyGlu 44
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                                         GGTCCTCCGGGGGCTCCTCCAGGACCGCCAGGTCCGCCTGGTCCCCCGGGACTG
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CCAGGCCCGAAAGGCGAT 114
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AR117066
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Ferrari,F.A. and Cappello,J.
Functional recombinantly prepared synthetic protein polymer
Patent: US 6140072-A 62 31-OCT-2000;
                                                                                                                                                                                                                                                                                               Unknown
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62 from patent US 6140072.
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Search completed: February 19, 2003, 23:07:44 Job time: 848.004 secs

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Maximum DB
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-Q-/G9n2_1/USPTO_spool/US09997610/runat_10022003_160823_23819/app_query.fasta_1.1635
-Q-/G9n2_1/USPTO_spool/US09997610/runat_10022003_160823_23819/app_query.fasta_1.1635
-DB-GenEmb1 -QPMT-fastap -SUFFIX=ye -MINMATCH-0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS-blts -STARF1 -END-1 -MATRIX=blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , X
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Delop 6.0 , E
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Result ŏ. 44440335544 44440335544 44440335544 44440335544 159 158 158 158 158 158 157 291.5 220 169.5 167.5 167.5 167.5 167.5 163.5 163.5 163.5 162.5 162.5 162.5 162.5 162.5 Score Match Query . . . . 68834 179303 206213 2435 731 1973 3216 3226 7 1028 7 10753 7 10753 7 10753 582 947 1134 200942 4443 4908 128133 173817 1265 5111 2005 11918 1385 259 2609 2609 2735 2235 2235 2415 2506 11700 145880 117089 182978 182978 19398 1980 3142 Length 10 Thu 5 CHKCX 59 10 AB667813S3 59 10 AB667813S3 6 AX332258 9 HSCOLBA1 PARCOLVIII 0 0 0 4 0 0 0 0 0 0 DB 10 9 9 30 10 10 0 MMCOLBA BTCOL10A1 0 MMAITXCOL 0 MMCOL10A AC119229 AC016087 AC021709 0 BC011061 0 MMAIXCOL HS10A1COL AC069222 HS302D9 AC120598 AC022883 0 AC067824 AF222861 AF269230 AC125396 AK074129 AX430953 HSCOLLX HSJ136014 AL355373 AF417206 HSCOLA1X G28608 AC012141 AX195207 AX358517 HSCOLX3 AX333243 HS302D9 TMSHP25 RNO131848 Ħ BC028770 D12974 Tamias asia ABORT779 Tamias asia ABORT779 Tamias asia ABORT779 Tamias asia AD13975 Tamias asia AJ131848 Rattus no D12975 Tamias asia AJ131848 Rattus no D12976 Tamias asia M13496 Chicken type ABORT97527 Human COLDA J05042 Rabbit type ABORT97527 Human COLDA J05042 Rabbit type ACOLT958 Homo sapi ACOLT959 Mus musculus X65977 M.musculus X65978 Homo sapi ACOLT909 Mus musculus X63013 M.musculus X63013 M.musculus X63013 M.musculus X63013 H.sapiens C X75580 Homo sapien AX333243 Sequence X60382 H.sapiens t X98568 H.sapiens Z82198 Human DNA Description Sequence Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
On Dec 13, 199 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS302D9 145880 bp DNA linear PRI 12-DEC-1999
HUMBAN DNA sequence from clone RP1-302D9 on chromosome 22 Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RP1-302D9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furth details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotated human repeat sequence elements (e.g. Alu). Whe sequence is ambiguous, there is an annotation using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridgeman,A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z82198.2 GI:6572207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the entire insert of clone RP1-302D9 end of clone CTA-282F2 is at 69682 in this sequence. end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (6 % No. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pCYPAC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eature key.
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                                                                                                                                                                                                                                                                                            /note="/
                                                        /note="AluSc repeat: 2684. .2981
                                                                                                  2350.
                                                                                                                                       1687
                                                                                                                                                                           1033. .1336
/note="AluSp repeat: matches 1.
1450. .1583
                                                                                                                                                                                                                                                      783.
                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP1-302D9"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                              /note="
                                                                                                                                                                                                                                                                                                                                                  /note="MER3 repeat: matches 144.
                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="22"
note="MLTlE repeat:
                                      'note="AluSq repeat: matches 2. .300 of consensus"
                                                                                                                                                                                                                                   /note="MER5A repeat: matches 26.
                                                                                                                                                                                                                                                                        /note="MER3 repeat: matches 1.
                                                                                                                                                       'note="MIR repeat: matches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .145880
                                                                                                                                                                                                                                                                                                            AluSx repeat: matches 1.
                                                                                                                  repeat: matches 2593.
  matches 116.
                                                                            matches 3.
                                                                                                                                                         .160 of consensus"
                                                                                                                                                                                                                                                                        .144 of consensus"
                                                                                                                                                                                                                                                                                                              .312 of consensus"
                                                                            .309 of consensus"
                                                                                                                    .2661 of
                                                                                                                                                                                             .299 of consensus"
                                                                                                                                                                                                                                   .187 of consensus'
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  .136
  of consensus"
                                                                                                                    consensus'
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true right
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    /note="MIR repeat: m
14589. .14679
/note="MIR repeat: m
14597. .15201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(10204.
/note="match: GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10179.
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5181. .5491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="THE1B repeat: matches
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/note="MLT1E repeat:
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/note="AluY repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                       13699
                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat:
13017. .13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 147.
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                                                                                                                       14061
                                                                                                                                                             13945.
                                                                                                                                                                             note="MIR repeat:
                                                                                                                                                                                                 /note="MIR repeat:
13806. .13919
                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 174.
                                                                                                                                                                                                                                                                                                                /note="match: STS:
13331. .13397
                                                                                                                                                                                                                                                        'note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="MIR repeat: matches 20.
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                                                                            AluY repeat: matches 1.
.14452
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                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 1988.
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                                                                                                                                                                                                                                                                                                                                                                             matches 63.
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                                                                matches 141.
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                          173.
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consensus"
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20513. .20666
/note="77 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:B14179"
19537. .20200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(18872.
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18713. .19133
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15304. .15399
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14868. .15040
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14616 .15060
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19251. .19719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16546.
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15669 .15727
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                                                                                                                                                                                                                                                                                                                                    'note≖"HUERS-P3 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MSTA repeat: matches
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Best Local Similarity:
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MetGlyValPheAlaCysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic
Sciences, Kitasato University, Laboratory of Molecular Biology;
1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takamatsu,N., Ohba,K., Kondo,J., Kondo,N. and Shi
Hibernation associated gene regulation of plasma
collagen-like domain in mammalian hibernators
Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
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D12974
D12974.1 GI:287467
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Tamias sibiricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HP-20; collagen-like domain; hibernation-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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KESTGVFNCVEPGNYHFSFDVELYHCKVKIGLMKNHIQVMEKHOLSKNEYENASGAMI
MPLRQGDKVWLEADVETEEPDQAKVVIYFSGFLISS"
99...157
                                                                                                                                                                                                                                                                                  /protein_id="BAA02351.1"
/db_xref="GI:287468"
/translation="WYDVWRLAIFVLMVNVLNDQVSCSGPPGPVGYPGVPGPRGP
                                                                                                                                                               /product="HP-20"
1238. .1243
                                                                                                                                                                                                                                                                                                                                                                                         89. .679
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/clone="pCM20-7"
                                                                                                                                                                                                                                                                                                                                      /product="HP-20"
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                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="liver"
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                                                                                                                                                                                                                                                                                                                                                                                 5121 bp
Tamias sibiricus gene for HP-20,
AB067779
AB067779.1 GI:15706341
                                                                                                                                                Submitted (04-AUG-2001) Motoharu Ono, Kitasatu
Department of Biosciences, School of Science;
Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                    Ono, M.
                                                                                                                                                                                                                          HP-20 gene
Gene 277 (1-2), 121-127
21488336
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                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                     Ono,M., Hosoe,Y., Azuma,S., Shoji,M.,
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                   Tamias sibiricus
                                                                                                                          Fax:81427789408)
                                                                                                                                                                                                                                                                                                                  Tamias
                                                                                                                                     E-mail:ms99805m@stu.sci.kitasato-u.ac.jp, Tel:81427789408
                                                                                                                                                                                                                (bases 1 to 5121)
                                                                                                                                                                                                                                                                            Takamatsu, N
                                                                                                                                                                                                                                                                 regulates the
                                     /note="synonym:Tamias asiaticus"
1518. .1684
/gene="HP-20"
join(1678. .1
                        join(1678.
                                                            /clone="lamdaCM20G1"
                                                                         /organism="Tamias sibiricus"
/db_xref="taxon:64680"
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Science; 1-15-1 Kitas
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SerSerPheAspValGluLeuHisHisCysLysValAsnIleTrpLeuMetArgLysGln 125
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                                                                                                                                                                                                                                                                                                                                                                                          ATCCAAGTCATGGAAAAGCATCAGCTCTCCAAAAACGAA
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Tamias asiaticus liver
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                     Hibernation-associated collagen-like domain in
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Takamatsu, N., Ohba, K.,
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/codon_start=1
/product="HP-20"
/protein_id="BAB68362.1"
/db_xref="GI:15706342"
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pgqpgaagrpgdpgpkgpsvkcpcrersaftvkfsgrlpppsepvvftevlyntqrdl
kastgvfncvepgnyhfsfdvelyhckvkiglmknhlqvmekhqlskneyenasgami
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(3), 1516-1521 (1993)
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                                                                                       GATGGTATCCAGGTCAGAGAGAAAGAAGCCCCAAGCCAATGACAGCTACAAACATGCAATG
                                                                                                                      LysGlnIleLeuAlaAsnLysGluGluIleSerLysGlnGlnSerIleGlnGluValThr
                                                                                                                                                    TACAATTTTGGCTTTGACATTCGACTGTTTCAGAGTTCTGTGAAGATCAGGCTCATGAGG
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Direct Submission
Direct Submission
Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic
Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic
Sciences, Kitasato University, Laboratory of Molecular Biology;
Sciences, Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax:0427-78-9403)
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/db_xref="GI:287470"
/translation="MPAQRGGALSMGAAGFWILVLSITSALADSNNQGNSEPCGPPGP
PGPPGIPGFPGAPGALGPPGPPGVPGIPGPQGPPGDVEKCSSRPKSAFAVKLSERPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="HP-25"
1983. .1988
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EKEAQANDSYKHAMGSVIMALGKGDKVWLESKLKGTESEKGITHIVFFGYLLYGK"
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/clone="pCM25-3"
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20310874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-DEC-1998) Wurtz T., Karolinska Institutet, Box 4064, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  failures of chondrocyte patterning and type X collagen expression Int. J. Dev. Biol. 44 (3), 309-316 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endochondral bone formation in toothless (osteopetrotic) rats:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Popoff,S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Odgren, P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marks, S.C. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norway rat.
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--IleGluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuPro
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VTGMPVSAFTVILSKAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="GYPGDPGLNGPKGNPGLPGPKGDPGVGGAPGLRGLVGPTGPKGV
PGHNGEAGPRGEPGIPGTRGPIGPPGIPGFPGSKGDPGKPGAPGPAGIVTKGLNGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="collagen alpha
/protein_id="CAA10518.1"
/db_xref="GI:4090263"
                                                                                                                                                                                                                                                                                                                                                                                                                  LYSSEYVHSSFSGFLVAPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                  HYKGTHYWYGLYKNGTPTMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLPNAESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:Q9Z1K4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="collOA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Rodentia;
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Huddinge, S-14104, SWEDEN
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D12976
D12976 D12976.1 GI:287471
HP-27; collagen-like domain; hibernation-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
Tamias asiaticus liver cDNA to mRNA, clone:pCM27-3
Tamias sibiricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Laboratory of Molecular Biology; 1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takamatsu, N., Ohba, K., Kondo, J., Kondo, N. and Shiba, T. Hibernation-associated gene regulation of plasma proteins with collagen-like domain in mammalian hibernators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax:0427-78-9403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takamatsu, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93180798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tamias
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1385)
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                                                                                                                                                                              65. .154
155. .70
                                                                                                                                                                                                            /translation="MYEAGKRASFMGGAGIWILALSYLMHVVCSETQGNPESCNVPGP
GGPPGMRGPPGTPGKPGPPGMRGPPGLFGPPGMYNCHSKGTSAFAVKANELPPA
PSQPYIFKRALHDAQGHPDLATGVFTCPVPGLYQFGFHIEAVQRAVKYSLMRNGTQVM
EREAEAQDGYEHISGTAILQLGMEDRVWLENKLSQTDLERGTVQAVFSGFLIHEN"
                                                                                                                                           /product="HP-27"
1369. .1374
                                                                                                                                                                                                                                                                               /protein_id="BAA02353.1"
/db_xref="GI:287472"
                                                                                                                                                                                                                                                                                                                                              /note="collagen-like domain
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:64680"
/clone="pCM27-3"
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                                                                                                                                                                                                                                                                                                            /product="HP-27"
                                                                                                                                                                                                                                                                                                                               /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                             tissue_type="liver"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 GCAGTGAAGGCAAATGAGCTGCCCCCAGCTCCCTCCCAGCCCGTGATCTTCAAGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 GGAAAACCAGGCCCACCAGGATGGAATGGTTTTCCAGGACTACCAGGGCCACCAGGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TCCTGTAATGTTCCAGGACCTCAAGGACCTCCAGGCATGCGGGGTCCCCCAGGTACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ATTTTGGCCCTGTCTGTACTAATGCACGTGGTGTTCTGAAACTCAAGGAAATCCTGAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 ValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 CCAGGC-----ATGACT---GTGAACTGCCACAGCAAAGGAACATCGGCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 LeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPheAlaCysArgValPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ThrValLysLeuSerGlyLysLeuProLeuProPheLysProIleIlePheThrGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 ThrGlyGluIleSerGluMetThrLysCysProCysProAspIleGluArgSerAlaPhe 61
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N Chicken type X collagen gene.
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M13496.1 GI:211699
collagen.
Chicken red blood cell DNA, cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGAAATGGCACCCAAGTCATGGAGAGAGAGAGCGGAGGCCCAGGATGGCTATGAGCAC
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                                                                                                                                                                                                           The developmentally regulated type X collagen open reading frame without introns
J. Biol. Chem. 261 (11), 5041-5050 (1986)
                                                                                                                                                                                                                                                                                                                                                             cDNA to mRNA, clone Gallus gallus
                                                                                                             [1] has as yet not determined the start codon of gene. The open reading frame starts at position several 'atg' codons (starting at positions 190, 310) following the 'taa' at position 163.
                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                 Ninomiya,Y.,
                                                                                                                                                                                                                                                                                                               Phasianinae; Gallus.
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nomiya,Y., Gordon,M., van der Rest,M.,
                                                                                                                                                                                                                                                                Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586
                 /cell_type="chondrocyte"
<1. .379</pre>
                                               /organism="Gallus gallus"
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                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                     GTTGCACTCTATAAAAATGGCTCCCCAGTCATGTACACTTATGATGAATACCAGAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGGAGAACCTGGCTTGCCAGGTCCCCCGGTCCTCCTGGTCCCCCTGGCCAATCCACA 1698
                                                                                                                                                                                                                                                                                                                    LeuMet --------ArgLysGlnIleLeuAlaAsnLysGluGluIleSerLys---
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Callosciurus caniceps DNA,
Callosciurus caniceps
Eukaryota; Metazoa; Chordat
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Callosciurus
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ELSGMSFMKAGANQALTGMPVSAFTVILSKAYPGATVPIKFDKILYNRQQHYDPRTGI
FTCRIPGLYYFSYHVHAKGTNVMVALYKNGSPVMYTYDEYQKGYLDQPQAVLSLISWR
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/protein_id="AAA48736.1"
/db_xref="GI:211700"
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AUTHORS
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AUTHORS
TITLE
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AX332258
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                                                                                                                                       GluGluIleSerLysGlnGlnSerIleGlnGluValThrTrpValLeuLeuLysAla 149
                                                                                                                                                                           GGACTGTTTCAGAGTTCTGTGAAGATAAGTCTCATGAGGAATGGTATCCAGATCAGGGAG
                                                                                                                                                                                                                                           GTGACCACTGGAGAGTTCAGCTATACCAACCCCGGTGTGTACAATTTTGGCTTTGACATT 271
                                                                                                                                                                                                                                                                                                               GGGTCCTTCCAGCCCATCATATTCAAGGAGTCTCTGTACAACCGGGAGGACCACTATAAC
                                                                                                                                                                                                                                                                                                                                                                                 TGCCCATCACCA-----CCAAAATCTGCCTTTGCCGTGAAGCTGAGTGAGCGTCCCCCA
                                                                                                     AAGCAAGCTCAAGCCAATGAAGGCTACAAACATGCATTGGGGGACTGTCATTGTGGCT
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 AX332258
Sequence
AX332258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-AUG-2001) Nobuhiko Taka
Department of Biosciences, School of
Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kojima,M., Shiba,T., Kondo,N. and Takamatsu,N. The tree squirrel HP-25 gene is a pseudogene Eur. J. Blochem. 268 (22), 5997-6002 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (E-mail:takamatu@jet.sci.kitasato-u.ac.jp, Tel:81427789408
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/product="HP-25"
39. .>559
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/gene="HP-25"
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/db_xref="taxon:64664"
/clone="lambda TS25G1"
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l of Science; 1-15-1 Kitasato,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Submitted (05-FEB-1991) B.R. Olsen,
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              X57527
X57527.1 GI:30081
collagen alpha 1 type III; extracellular matrix
                                                                                                                                                                                  HSCOL8A1 mRNA for alpha 1(VIII) collagen
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Location/Qualifiers
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Patent: WO 0194629-A 2767 13-DEC-2001;
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                                Olsen, B.R.
                                                                                                  Homo sapiens
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                                      AspIleGluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLys 74
                                                                                     GGCGTGAAACCCCCCCATGCTACGGGG------GCTAAGAAAGGCAAGAATGGAGGGCCA 1833
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GMPGMPGKPGAMGMPGAKGEIGQKGEIGPMGIPGPQGPPGPHGLPGIGKPGGPGLPGQ
PGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGVKGPPGMHGLPGPVGLPGVGKPGV
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/translation="MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGIKPLPPQIPPQMPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHLQYGKEYPHLPQYMKEIQPAPRWGKE
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EQGLPGLPGAPGLPGIGKPGFPGPKGDRGMGVPGALGPRGEKGPLGGSPGLEGSSPGEP
GLPGLPGBMGPPGAIGFPGPKGEBGIVGPGGPFKGEPGLJQGPPGKPGFLGGEVGPPG
MRGFPGPIGPKGEHGQKGVPGLLGVPGLLGFKGEPGIPGDQGLQGPPGIPGIGGPSGP
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/codon_start=1
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/db_xref="GI:30082"
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/clone="YMh801"
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/chromosome="3"
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Rabbit type VIII collagen alpha-1 chain
J05042
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Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamaguchi, N., Benya, P.D., van der Rest, M. and Ninomiya, Y.
The cloning and sequencing of alpha I(VIII) collagen cDNAs
demonstrate that type VIII collagen is a short chain collagen and
contains triple-helical and carboxyl-terminal non-triple-helical
domains similar to those of type X collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer-readable copy of sequence [1] kindly submitted by Y.Ninomiya 23\text{-AUG-}89.
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Yamaguchi, N., Benya,
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 264 (27), 16022-16029 (1989)
                                                                                                                                            536
                                                                                                                                                                                                                                                                                                           /product="alpha-1 (VIII) collagen"
719 c 768 g 392 t
                                                                                                                                                                                                                                     EPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYL
                                                                                                                                                                                                                                                   PFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNN
                                                                                                                                                                                                                                                                   PPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAAKKGKNGGPAYEMPAFTAELTA
                                                                                                                                                                                                                                                                                IRGLPGP1GPKGEPGLPGPPGFPGVPGLLGPKGEPG1PGDQGLQGPPG1PG1TGPSGP
IGPPG1PGPKGEPGLPGPPGFPGVPKGEPG1PGDQGLQGPPG1PG1TGPSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                        /note="alpha-1 (VIII) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAA31204.1"
/db_xref="GI:164896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MAVPPGPPQLLQVLLTISLGSIRLIQAGAYYGIKPLPPQIPPQM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha-1 (VIII) collagen precursor
   2.03e-05
163.50
44.20%
32.61%
20.70%
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   Indels:
Gaps:
                                 Mismatches:
                                              Matches:
Conservative:
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Homo sapiens, clone MGC:9568
BC013581
BC013581.1 GI:1548Rana
                                                                                                                         Series:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                1. .2506
/tissue_type="Lung, large cell carcinoma"
                                                                              Location/Qualifiers
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1840 GGCCAGCCTGGCCTCCCAGGCCCCCAGGCCCTCCAGGGCCTCCAGGGCCCCCCAGCTGTG 1899
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                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                             es: IRAK Plate: 14 Row: a Column: 8 clone was selected for full length sequencing because it at the following selection criteria: matched mRNA g1: 996
                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:9568 IMAGE:3875911"
                                                                                                                                                                                                                                                                                                                                                                                                     http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
4., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp mRNA
IMAGE:3875911,
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATGCCTGCATTTACCGCCGAGCTAACCGCACCTTTCCCACCGGTGGGGGCCCCCAGTG 2136
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                                                                                                                                                                                                                                                                              ---ValAsnIleTrpLeuMetArgLysGlnIleLeuAlaAsnLysGluGluIle 133
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                                                                                                      Homo sapiens
BAC Library)
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                    Homo sapiens
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sapiens
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PFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNN
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GLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPGFKGEPGLQGFPGKPGFLGEVGPPG
MRGLPGPIGPKGEAGQKGVPGLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGP
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PGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGVKGPPGMHGPPGPVGLPGVGKPGV
TGFPGPQGPLGKPGAPGEPGPQGPIGVPGVPGPPGIPGIGKPGQDGIPGQPGFPGGKG
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238. .2472
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Bunday, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T. E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
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Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N.,
Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N.,
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                                                                                                            Direct Submission
Submitted (29-MAR-2002) Human Genome Sequencing Center, Depar
Submitted (29-MAR-2002) Human Genetics, Baylor College of Medicine,
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Direct Submission
Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Bavlor Plaza, Houston, TX 77030, USA
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Baylor Plaza, Houston, TX 77030, USA
On Mar 1, 2002 this sequence version replaced gi:18958589.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-MAY-2000) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 117000)
                                                                                 of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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# ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

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                                           complement(9345.
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                                                                                                                                                               complement(5611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-383I23"
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               c_family="Alux"
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lement(5800
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family-"Charlie1b"
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Best Local Similarity:
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                                                                                                                 .72209 ATGCCCCCTACACCACCACCAGGGAGAGTATCTGCCAGATATGGGGCTGGGAATTGAT 72150
72089 GAGATGCCTGCATTTACCGCCGAGCTAACCGCACCTTTCCCCACCGGTGGGGGCCCCAGTG 72030
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                                                          GGCGTGAAACCCCCCATGCCTACGGGGCTAAGAAAGGCAAGAATGGAGGGCCAGCCTAT 72090
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/rpt_family="L2"
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complement(22803. .231
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                                                                                                                                                                                                                                                                                                                     FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ValAsnIleTrpLeuMetArgLysGlnIleLeuAlaAsnLysGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGTGAGGTCCCTGGTGTCTACTACTTTGCATACCACGTT-----CACTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaCysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeuHisHisCysLys 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGCAACGTGTGGGTT------GCTCTATTCAAGAACAACGAGCCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk

On Dec 13, 1999 this sequence version replaced gi:3164067.

During sequence ussembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSSs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp;, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z82198.2 GI:6572207
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                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP1-302D9 end of clone CTA-282F2 is at 69682 in this sequence. The end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bridgeman,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS302D9
                                                                                                                                                                                                                                                                                                                                                                                                                  details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RP1-302D9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                teature key.
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                                                                                                   246.
/note="MER3 repeat: matches 1.
783. .933
                                                                                                                                                188.
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                     /note="MER3 repeat: matches 144.
                                                                                                                                                                       /clone_lib="RPCI-1"
                                                                                                                                                                                             /clone="RP1-302D9"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                        note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                      chromosome="22"
                                                                                                                                                                                                                                                                                               .145880
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                           .144 of consensus"
                                                                                                                          .209
                                                                                                                          of.
                                                                                                                       consensus'
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/note="L2
6647. .668
                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 15.
9521. .9679
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1033. 1336
/note="AluSp repeat: matches 1.
1450. 1583
                                              13331
                                                                                                                                                                                                                                                                                                                                                                                                                                        9283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MADE1 repeat: matches 23.7482...7754
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                                                                                                                                                                                             /note="match: GSS: 10784. .11201
                                                                                                                                                                                                                         /note="MIR repeat: matches 79. 10718. .11310
                                                                                                                                                                                                                                                                                                                                 complement(10179. . /note="match: GSS:
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                                                                            13017
                                                                                                                                                                                                                                                                                 complement(10249.
                                                                                                                                                                                                                                                                                                                  complement (10204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9110.
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                                                                                                                                                                   11838.
                                                                                                                                                                                                                                                                                                     /note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                             /note="MSTB repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                           /note="FAM repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJb repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Alusx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MADE1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MLT1E repeat: matches 359. .568 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="THE1B repeat: matches 3. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3653. .3928
/note="MLT1E repeat: matches 136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluY repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MLT1E repeat: matches 116. .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSq repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSc repeat: matches 3.
13398. .13698
/note="AluSp repeat:
                               /note="MIR repeat: matches 174.
                                                            note="match:
                                                                                          /note="MIR repeat:
                                                                                                                       /note="L2
                                                                                                                                                                               note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="MIR repeat: matches 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2660
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                                                                                                        .12642
                                                .13397
                                                                                                                                 MIR repeat: matches 20.
                                                                                                                                                                    .11946
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                                                                                                                       repeat:
                                                                                                                                                                                                                                                                        GSS:
                                                                                                                                                                                 GSS:
                                                                                                                                                                                                                                                                                                  Em: B56592"
.10728)
: Em: AQ701486"
                                                                                                                      matches 1988.
                                                                                                                                                                                                                                                                      .10706)
Em:AQ225495'
                                                            Em: G49301"
                                                                                          matches 63.
                                                                                                                                                                               Em: B43656"
                                                                                                                                                                                                           Em: B14024"
                                                                                                                                                                                                                                                                                                                                                 10678)
matches 1.
                                                                                                                                                                                                                                                                                                                                                                                           .161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                        .144 of consensus
                                                                                           .241 of consensus"
                                                                                                                                                     .137 of consensus"
                                                                                                                                                                                                                                            . 150
                                                                                                                                                                                                                                                                                                                                                               .425 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    .262 of consensus"
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                                                                                                                       .2275
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                               .244 of consensus"
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   .302 of
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 76. 13806. .13919
                                                                                                                                                                                                         consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(18872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1B repeat: 15728. .16027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14589
                                                                                                                                                                                                                       /note="MER66-internal repeat: matches 2186.
                                                                                                                                                                                                                                                                                                                  /note="AluSg1 repeat: matches 1. .306 of consensus"
21239. .21553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER66-internal repeat: matches 4919. .4993 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MLT1B repeat: matches 178. .390 of consensus"
16546. .16854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14368
                                                                                                                                       /note="MER66-internal repeat: matches 1210.
                                                                                                                                                                                                                                                  /note="THE1B repeat: matches 1. .364 of consensus"
22302. .22537
                                                                                                                                                                                                                                                                                                /note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
                                                                                                                                                                                                                                                                                                                                                                     /note="77 copies 2 mer tt 70 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ005063"
19251. .19719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSc repeat: matches 1. .299 of consensus"
16028. .16245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSg1 repeat: matches 2.
15669. .15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MLT1B repeat: matches 1.
15490. .15662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS:
14616. .15060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluY repeat: matches 1.
14368. .14452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 24.
14061. .14367
                                                                                       'note="MER66-internal repeat:
                                                                                                                                                                          'note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                    'note="33 copies 2 mer ta 68 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"HERVFH21 repeat: matches 4657. .5784 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER66-internal repeat: matches 4548. .4919 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MSTA repeat: matches 2. .29 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="L2 repeat: matches 2112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ370601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="MIR repeat: matches 77.
0.00201
162.50
50.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193. .18712
>te="AluJb repeat: matches 1.
13. .19133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te="match: GSS: Em:B14179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .18323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .18392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .15040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 мік repeat: matches 49.
.15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIR repeat: matches 141.
.14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 20290
                                                                                                                                                                                                                                                                                                                                                                                       20666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 1.
Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .19230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Em: AQ553482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 119. .178 of
                                                                                       matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .189 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .174 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .233 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .301 of consensus"
                                                                                                                                                                          .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .99 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           consensus"
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pocus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
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                                                                                                   MuznyD.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burchl,K.L., Byrd,N.C.,
Chen,G., Chen,R., Check,D., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Ding,Y., Dinh,H.H.,
Dathwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Garza,N., Gill,R.,
Gothsi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Gavara,W., Gunrartne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Kratsyon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Jackson,L.E.,
Li,J., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
Lozado,R.J., Lu,X., Lucier,R., Lucier,R., Luna,R., Ma,J.,
Mansey,E., McLeod,M.P., Meador,M., Martinez,E.,
Massey,E., Mawhiney,E., Wcleod,M.P., Meador,M., Morris,S.,
Moser,M., Natchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Mall,D., E., Wockenkwo,S., Oguh,M., Okwuon,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCTGTTTCAGAGCTGTGCAAATGTGGGTATTATGAGGAATGGCATCCATATGAGAAAT 90660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLeuHisHisCysLysValAsnfleTrpLeuMetArgLysGlnIle---LeuAlaAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCTGGTGAAGGATTCACCTGTACCATCCCTAGTGTGTACCACTTTGGTTTTTGAATTT 90720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAlaMetGlyValPheAlaCysArgValProGlyAsnTyrTyrSerSerPheAspVal 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCCCTTCTAGCCCATTGTCTTCAAGGAAGCCCCTTTATAATACTCAGTTCCATTTCCAT 90780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuProPheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACATGCTGTGGCCAAGGATGGCTATGAGCAGGAA 90624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGluGluIleSerLysGlnGlnSerIleGlnGlu 141
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
                                                                                    Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC120598.3 GI:21902634
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Sodergren, E., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Sutton, A., Taylor, T., Talfrod, B., Thomas, N., Thomas, S., Tansey, J., Taylor, T., Talfrod, B., Thomas, N., Thomas, S., Usaguez, L., Vera, V., Villalon, D., Vinson, R., Wang, C., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Warg, S., Warlinson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAY 2002) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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On Jul 18, 2002 this sequence version replaced gi:20564266
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Direct Sub
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

(see http://www.hgsc.bcm.tmc.edu/do
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Contact: hgsc-help@bcm.tmc.edu
------- project Information
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-Q-cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23843/app_query.fasta_1.1635
-Q-cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23843/app_query.fasta_1.1635
-DB-EST -QFMT-fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-SOO -MINIEN-0 -MAXLEN-2000000000
-USER-US09997610_eCGN_1_1_1871_erunat_10022003_160823_23843 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DBV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BE420422 LOCUS DEFINITION		44 45		41 41	39	37		C 33	32	30	28 29	27	25.5	c 23	21 22	20		c 16	րդ դ Մ 4	13	311	1 0 9	8 ~	1000	J 42-	ωı	بر د	Result No.
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                    ProProIleArgPheGlnLysIleTyrGlyAsnProTrpMetProArgGlnLysPheAla
                                                                                         GlnLeuProSerGlyValGluProValGlyAlaLysLysSerArgIleGluValTrpGlu
                                                                                                                                           GAAAGGGGCCCAACATAGAGCTCGGATTGTGGCTTCAGAGGGTGCAAGCTGTAAGCCTTGG
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                                                                                                                                                                                                                                                                                                                                                          CCCCAAGACAATGGGGAAAATGTCTCCAGGGCATGCCAGAGGTCTTCACAGCAGCCCCTC
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CCTCTGCCTAGATTTCAGAAGATGTATGGAAATGCCTGGATGCCCTGGCAGAAGTCTGCT
                                                                      CAGCTTCCATGTGGTGTTGAGCCTGCCAGTGCACAGAAGTCAAAAATTGGGGTTTGGGAA
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Contact: xingwu Lu,liangxian Cui,yonghai
Department of Biochemistry
Institute of Basic Medical Science, Pekin
DongDan SanTiao 5, Beijing, P.R.C, 100005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length and coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 38 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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                     analysis
This clor
                                                   Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNI at: http://image.llr Series: IRAL Plate: 14 Row: d Column: 7 This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens, Similar to IMAGE:3831313, mRNA.
                                                                                                                                                                                                                              CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. COT DNA Sequencing by: Institute for Systems Bi http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-MAR-2001) National Institutes of Her
Gene Collection (MCC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                       contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey,
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                   clone has the following problem:
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SerThrAspThrGlnCysGlnProValLysAlaAlaGlyMetGluSerValProTyrLys
                                     ProSerSerArgLeuGlnLysGlyArgSerThrAspSerLeuGlnHisValProGluLys
                                                                      GAGCCCCCACACAGAATCCCTACTGAGGCACCACCTAGTGGAGCTGTGAGAAAAGAGCCA
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/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="TH10B-R"
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Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking Union Medical College
DongDan SanTiao 5, Beijing, P.R.C, 100005
Tel: 86-010-65296951
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32-1514 human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full cDNA sequence.
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                                                                                                                                                                                                                                                                            /clone_lib="human B lymphocyte cDNA library"
/tissue_type="bone marrow"
/note="organ; tonque; Vector: pAMP10; mRNA made from
/note="organ; tonque; Vector: pAMP10; mRNA made from
tongue epithelium, cDNA made by oligo-dT priming.
Non-directionally cloned into UDG sites. Size-selected on
agarose gel, average insert size 500 bp. Primary library.
cDNA Library Preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research
56:5380-5383."
341 c 398 g 395 t
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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High quality sequence stop: 713
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: testtis; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
a 228 c 254 g 191 t
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/db_xref="taxon:9606"
/clone="IMAGE:5583427"
/clone_lib="NIH_MGC_92"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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BQ893011.1 GI:22285025
EST.
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AGENCOURT_8122304 Lupski_dorsal_root_ganglion
clone IMAGE:6179271 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R.
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCGACGCGTCGG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                              /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
                                                                                                                                 /dev_stage="adult,
/lab_host="DH10B"
                                                                                                                                                                                                   /clone="IMAGE: 6179271"
                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                            /sex="male"
                                                                                                                                                                                     /clone_lib="Lupski_dorsal_root_ganglion"
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                                                                                                                                 TyrLeuLeuHisCysHisAspLeuAspValArgHisGlyValLysArgAspHisPheGly
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                                                                                                                                                                          AGGAGGGAGACTGTACCCTGCAAAGCCACAGGGGCAGAGCTGCTCAAGACCATGGGAACC
                                                                                                                                                                                                  GlyMetGluSerValProTyrLysThrValValAlaGluLeuThrLysThrValGlyIle
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                                                                                                                  TACCTCTTGTATCAGCATGACCTGNATGTGAGACATGGAGTCAAAGGAGAACATTTTGGA
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                                                                                          ProGlySerLeuCysCysValGlnProArgAspLeuValProCysValPro------
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AGENCOURT_6478314 NIH_MGC_72 Homo sapiens cDNA clone
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1036)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, A
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMv-SPORT6;
Site_2: Sall; Cloned unidirectionally. P
Average insert size 2 kb. Library const
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239 c 294 g 247 t 2 others
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/clone="IMAGE:5563049"
/clone_lib="NIH_MGC_72"
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AGENCOURT_6465359 NIH_MGC_72
5', mRNA sequence.
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/organism="Homo sapiens"
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/clone="IMAGE:5539381"
/clone_lib="NIH_MGC_72"
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                                LeuGlnHisValProGluLysSerThrAspThrGlnCysGlnProValLysAlaAla---
                                                         GGAGCTGTGAGAAAAGAGCCACCATCCTCCACACCCCAGAATGATAGATCCACCAACAGC
                                                                    ArgAlaValArgArgSerProProSerSerArgLeuGlnLysGlyArgSerThrAspSer
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                    TTGCACCATGCACCCTGGAAAGCCGCAGACATTCAACACCAGCCCGGGGAAGCAGCCAAA
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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                                                                                                                                                                                                spSerLeuGlnHis-ValPro-GluLysSerThrAspThrGlnCysGlnPro 357
                                                                                                                                                                                                                                      GTGGAGCTTGTGAAAAAGAGGGCCACTGTCCTCCAGACCCCCANAAATGGTAGATCCACTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalia
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies,
CDNA Library Preparation: Life Technol
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603021014F1 NIH_MGC_114
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 870)
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Primates;
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    Technologies,
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                                                                                Hominidae;
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IMAGE:5191803 5',
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                                                                                                                                                                                                                                                                                                                            alGlyAlaLysLysSerArgIleGluValTrpGluProProIleArgPheGlnLysIleT
                                                                                                                                                                                                                                                     CTGTGGCTTCAGAGGGTGGAAGCTCTAAGCTTTGGCAGCTTCCACGTGGTGTTGAGCCTA
                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11479 row: k column: 04
{\tt erGlyAlaProSerSerArgAlaValArgArgSerProProSerSerArgLeuGlnLysG}
                                    CCTCTGCTGGAGCAGTGCAGAAGGAAAATGTGGGATCGGAGCCCCGACAGAGAGTCCATA
                                                         hrSerAlaArgValValGlnLySGlyAsnValGlyTrpGluProProHisArgValProS
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/db_xref="taxon:9606"
/clone="IMAGE:5191803"
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/lab_host="DH10B"
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13596 row: b column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
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1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
Email: cgapbs-r@mail.nih.gov
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                               257
                               a
                           5'-GACTAGTTCTAGATCGCGAGCGGCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
                                                                                                                         /note-"vector: pCMV-SPORT6 (Life Technologies); Si
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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                                                       GGGACCCACCCTCTT
                                                                                                            CACCCAGGGAGGGAGGCTGTACCCTGCAAAGCCACAGGGGGGTGGGACAGCCCAAGACTAT
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                       GlnLysPheAlaValGlyValGlySerSerTrpArgThrSerAlaArgValValGlnLys 304
                                                                                                            GluValTrpGluProProIleArgPheGlnLysIleTyrGlyAsnProTrpMetProArg
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                                                                                                                                                                                                                                                               CCAGCCATGGGTGAAAGGGACCAACATAGAGCTCAGACTGTGGCTTCAGAGAGTCCAAGC 124
AAGAAGGTCGCTACAGGGGCAGGGCACTCATGGAGAACCTCTGCTAGGACAGTGCAGAAG
                                                                                       GGAGTTTGAGAACCTCCGCCTAGATTTCAGAGGATGTATGGAAATGCCTGGATGTCCAGG
                                                                                                                                                                            CCCAAGTCTTGGCAGCTTCCACATGGTGTTGAGCCTGCAAGTGCACATAAGTCAAGAATT
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BM554723
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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/note="organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oliqo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5, adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
a 251 c 295 g 256 t
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AGENCOURT_7766790 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6015590
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13211 row: o column: 15
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Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 1080)
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                                                                     /clone="IMAGE:6015590"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 304 c 221 g 316 t
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/db_xref="taxon:9606"
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TITLE
                    SerGlyAlaProSerSerArgAlaValArgArgSerProProSerSerArgLeuGlnLys
                                                                                                ThrSerAlaArgValValGlnLysGlyAsnValGlyTrpGluProProH1sArgValPro
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ACTGAGGCACTGCCTAGTGGAGCTATGAGAAAAGGGCCATGGTCCTCCAGACCCCAGAAT
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This clone (DKFZp68080612) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from 5. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
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/tissue_type="human skeletal muscle
/dev_stage="adult"
/lab_host="0H10B"
/note="Vector: pTriplEx2; Site_1: S
cDNA-collection"
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MCC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Contact: Robert Strausberg,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DH108 (phage-resistant)"
/note="Organ: skin; Vector: pcMv-SPORT6; Site_1:
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/clone_lib="NIH_MGC_72"
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/db_xref="taxon:9606"
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 998)
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Qy 289 Db 481	Qy 269 pb 421	Qy 249 Db 361	Qy 235 Db 301	Qy 221 Db 241	Qy 201 Db 181	Qy 181 Db 121	Qy 161 Db 62	Qy 142 Db 2	us-09-997	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	BASE COUNT	FEATURES Sour	TITLE JOURNAL COMMENT
IGlyValGlySerSerTrpArgThrSerAlaArgValValGlnLySGlyAsnValGlyTr 309 	OPTOIleArgPheGlnLysIleTyrGlyAsnProTrpMetProArgGlnLysPheAlaVa 289	nLeuProSerGlyValGluProValGlyAlaLysLysSerArgIleGluValTrpGluPr 269 	AsnSer-AlaValalaSerGluGlyAlaSerProLysProTrpG1 249 :::	CysCysValGlnProArgAspLeuValProCysValProVal234 	ysSerLeuAlaTrpArg-ProArgArgLysTrpPheCysGlyThrGlyProGlySerLeu 220 	roGlnAspAsnGlyGluAsnIleSerTrpThrCysGlnArgSerSerGlnGlnSerIleL 201 	luGlyLysPheLysLeuAlaAlaGluIleCysIleCysAsnGluGluLeuAsnValAsnP 181 	LysSerSerGluAsnLeuHisProAspAsnValIleLysLysLysAsnProPheSerG 161 	-610-2_COPY_18_459 (1-442) x BM903785 (1-998)	: Scores: 5.19e-56 Length: 998 : 731.00 Matches: 183 :imilarity: 64.65% Conservative: 20 :l Similarity: 58.28% Mismatches: 83 :ch: 30.26% Indels: 30 :ch: 5.19e-56 Length: 998 : 183 : 183 : 183 : 184 : 185	// Julyanish nome Sapiens // Ab_xref="taxon:9606" // Clone="IMAGE:5492244" // Clone="IMAGE:5492244" // Clone="IMH_MGC_67" // Lissue_type="retinoblastoma" // Lab_host="DHIOB (phage-resistant)" // Lab_host="DHIOB (phage-resistant)" // Note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1; // Note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1; // Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies." Technologies." Technologies." Technologies."	http:// Plate: High qu	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Search completed: February 19, 2003, 19:35:44 Job time: 3455.83 secs

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Command line parameters:

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-O-/ggn2_1/USPTO_Spool_US09997610_runat_10022003_160823_23819/app_query.fasta_1.1635
-DB-GenEmb1 -OFMT-fastap -SUFFIX-rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100.-THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-Pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09997610_eCGN_11_13965_@runat_10022003_160833_23819 -NCPU-6 -ICPU-3
-NO_MAND_-LARGEQUERY -NEC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6 -FGAPEXT-7
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gb_ph: *
gb_pl: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_ba:*
                              em_mu:*
em_om:*
em_or:*
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gb_vi:*
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                                                                                                                                                                   em_fun:*
em_hum:*
em_in:*
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No.
RESULT 1
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Match Length DB
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em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
                                      em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
em_htg_vrt:*
em_sy:*
                                                                                                  em_htg_mus:*
                                                                                                             em_htg_other:*
                                                                                                                         em_htg_inv:*
                                                                                                                                                em_vi:*
                                                                                                                                      em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

ij

Description

N	9 AL596285	110820	48.9	18	44	C
74339 Homo s	AC07433	53	8.9		43	C
4023 Homo s	AC02402	598	9.0	18	42	C
079343 Human	CNS00M8	73	9.0	118	41	
001695 Homo	AP00169	400	9.0	184.	40	
22312 Homo	AC02231	827	9.0		39	
1594 Homo s	AP00159	000	9.0	1184.5	38	
0144 Homo	AP00014	2	9.0		37	
00230 Homo	AP0002	4	9.0	.~	36	
109967 Homo s	HS22F01	Ξ	9.1	5	ა 5	
807742 Human	AL80774	Ň	9.1	σ.	3 4	
091005 Homo	AC09100	168502	9.1	1187	ω ω	C
87699 Homo	AC08769	9	9.3	119	32	
77 Homo	AC02557	2	9.3	1190.5	31	
39 Homo sa	AC01663	2	9.3	1192	30	C
32 Homo sa	AC01663	5	9.3	19	29	C
34 Homo sa	AL35363	7	9.4	1193	28	
to	AC00815	8	9.4	119	27	
98 ното	AC11249	5	9.4	93.	26	
75 Homo	AC01607	743	9.4	193.	25	C
3098 Homo	AC02309	851	9	1194	24	C
Homo s	AC00304	667	9.4	119	23	
8962 Human DN	-	245	9.4	1194.5	22	O
luman D	HSU212C	0	9.5	119	21	
	AC	866	9	1195.5	20	
Homo	AC01709	030	9 .	1198	19	
Homo	AC01024	174293	9.6	1198	18	
Homo	AC00881	74	20 0	1198	17	(
_	AC01347	170723	9 (	1198	16	3 (
Homo	AC01028	. u	מים	1198	л . - Н	) (
Homo	AC02642	900	, סינ	110	1 2	3 (
	AC01671	875	y (		٠ ۱	3 (
Homo	AC01133	л ( л (	, u	100	۱ <del>۱</del>	) (
AC093536 Homo sap	AC00353	900	٥.	1200	1 5	3 (
HOMO GAD	AC00004	9 .	7 1	2 5	5 ,	3
2201 Human D	HS345P1	377	9 0	20	٥٥	
139216 Human DN	AL13921	2	0	1207	<b>20</b>	
106901 Homo	AC10690	913	0.0	120	7	
044889 Homo	AC04488	897	0.4	217.	თ	C
123595 Homo	AC1235	748	0.4	217.	տ	
008799 Homo s	AC00879	23(	0.4	217.	4	
087500 Homo s		716	50.4 1	1218.5	w	
AC025233 Homo sap	AC02523	615	0.4	218.	N	ဂ
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ALIGNMENTS

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SOURCE
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On Dec 13, 1999 this sequence version replaced gi:3164067.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr22
RPI-302D9 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For furth
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSs, (
Z82198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bridgeman, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s sequence is the entire insert of clone RP1-302D9 The true left of clone CTA-282F2 is at 69682 in this sequence. The true right of clone CTA-415G2 is at 55167 in this sequence.

Location/Qualifiers
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                                                                                             /note="L
2350. .2
                                                                                                                             /note="MIR repeat: 1687. .1757
                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 1.
572. .759
                                                                                                                                                                                                                                                                                                                                                     188.
                                                       /note="AluSc repeat:
2684. .2981
                                                                                                                                                                                                                                                                                                                                                                 _clone_
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                   1033. .1336
/note="AluSp repeat: matches 1.
1450. .1583
 'note="MLT1E repeat:
                    /note="AluSq repeat: 3323. .3343
                                                                                                                                                                                                                    note="MER5A repeat: matches
                                                                                                                                                                                                                                                          note="MER3 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                               /note="MER3 repeat: matches 144.
                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP1-302D9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .145880
                                                                                                                                                                                                                                             . 933
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                                                                                                                                                                                                                                                                                                                                                                     _lib="RPCI-1"
                                                                                                            2 repeat: matches 2593.
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8914.
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3653, 3000
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                                                                                                                                          /note="MIR repeat: 13945. .14060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(10249.
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                                    /note="MIR repeat: matches 141.
14589. .14679
                                                                                       /note="AluY repeat:
                                                                                                            /note="MIR repeat:
14061. .14367
                                                                                                                                                                                    13806.
                                                                                                                                                                                                                      13699.
                                                                                                                                                                                                                                                                                                                                    13017
                                                                                                                                                                                                                                                                                                                                                note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                     12444.
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10312. .10383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat:
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/note="MADE1 repeat: matches 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJb repeat: matches 1.
6369. .6485
/note="L2 repeat: matches 2579.
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                                                                                                                                                                                                                                       'note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 174.
                                                                                                                                                                                                                                                                                                               note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"MIR repeat: matches 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="AluJb repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note≔"AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MADE1 repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ="L2 repeat: matches 2579.
.6685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8060
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18324. .18392
/note="MER66-internal repeat: matches
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15728. .16027
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20317. .20382
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19537. .20290
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16546. .16854
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15669. .15727
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15304. .15399
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14616. .15060
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18713. .19133
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Sequencing vector: plasmid; 10%
Sequencing vector: plasmid; 10%
Chemistry: Dye-primer ET; 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 14558 bases at least Q40
Consensus quality: 149743 bases at least Q30
Consensus quality: 152625 bases at least Q20
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                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161575 bp DNA linear HTG 07-
Homo sapiens chromosome 17 clone RP11-333E1, WORKING DRAFT
SEQUENCE, 27 unordered pieces.
                                                                                                                                                                                                                                                                                                   Insert size: 176000; agarose-fp
Insert size: 158975; sum-of-contigs
Quality coverage: 3.48 in Q20 bases; agarose-fp
Quality coverage: 3.75 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0333E01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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2 (bases 1
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be preserved.
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Jul 7, 2000 this sequence version
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                                                                                                                                                                                                         be updated with the finished sequence
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AGTTTTATGAGGGAAGCAGAGCATAAAAGTTCAGAAAATTTGCAGCCTGAGAATGTGATA
                                                      SerPheIleArgGluAlaGluHisLysSerSerGluAsnLeuHisProAspAsnValIle 153
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9042: contig of 11488 bp in length
90522: gap of unknown length
100763: contig of 10241 bp in length
11067: contig of 10241 bp in length
111672: contig of 10809 bp in length
111772: gap of unknown length
1126855: contig of 15083 bp in length
126855: gap of unknown length
126955: gap of unknown length
142557: contig of 15602 bp in length
142557: contig of 18918 bp in length
161575: contig of 18918 bp in length
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                                                                                                                                                                                         171625 bp
Homo sapiens chromosome 17 clone
IN PROGRESS ***, 2 ordered pieco
ACO87500
                                                                                                                                                 HTG;
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AC087500.15
                           Birren, B., Nusbaum, C. and Lander, E.
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        Homo sapiens
                                             (bases 1 to 171625)
                                                                                                                                               HTGS_PHASE2;
        sapiens chromosome 17, clone RP11-333E1
                                                                                                                                             HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                      ordered pieces
                                                                                                                                                                                                                          clone RP11-333E1 map 17,
                                                                                                                                                                                                                            *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                             On Aug 13, 2002 this sequence version replaced gi:22122948 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zembek,L., Zimmer,A. and Zody,M.
                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
the accession number will be preserved.

1 27961: contig of 27961 bp in length
27962 28061: gap of 100 bp
28062 171625: contig of 143564 bp in length.
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                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.
                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPewan, P., McMernan, K., McPewan, P., McMernan, K., McPewan, P., McMernan, K., McPewan, P., McMernan, C., McMernan, C., McCarthy, M., McPewan, P., McMernan, C., H., McPewan, P., McMernan, C., H., McMernan, C., Norman, C., H., McMernan, C., Norman, C., H., McMernan, P., Peterson, K., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Royando, C., Retta, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Storauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travis, N., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Mann, D., Ye, M.J., Young, G., Zainoun, J., Mann, D., Ye, M.J., Young, G., Zainoun, J., McMan, M., McMan, D., Ye, M.J., Young, G., Zainoun, J., McMan, M., Ye, M.J., Young, G., Zainoun, J., McMan, M., McMan, M., McMan, M., McMan, M., McMan, M., McMan, M., McMan, McMan Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Gitzhugh, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T., Anderson, S.

Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 171625)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Neldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Pierre, N., and Zody, M.

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GGAGCTGTGAGAAGAGGGCCAATGACCTCCAGACCCCAGAATGGTAGATCCACCTACAGC
                ArgAlaValArgArgSerProProSerSerArgLeuGlnLysGlyArgSerThrAspSer 342
                                                            CAGAAGGGAAATGTGGGGTCGAAGCCACCATATGGAGTCCCTACTCGGGCACCTTCTAGT
                                                                            GlnLysGlyAsnValGlyTrpGluProProHisArgValProSerGlyAlaProSerSer 322
                                                                                                                         CCCAGCCAGAAGTTTGCTGCAGGGGCAGGGATCTCATGGAGAACCTCTGCTAGGGCACTG
                                                                                                                                             ProArgGlnLysPheAlaValGlyValGlySerSerTrpArgThrSerAlaArgValVal
                                                                                                                                                                                                                                                   GGGTGCCCTAAGCCTTGGCAGTTTCCACATGGTGTTGAGTCTTTAGGTACACAGAAGTCA 137252
                                                                                                                                                                                                                                                                   AlaSerProLysProTrpGlnLeuProSerGlyValGluProValGlyAlaLysLysSer 262
                                                                                                                                                                                                                                                                                                                                                                             GGGCCAGGCCCAGGGTCCCAATGCTGTCCCAGCCTAGGGACTTGGTGCGCTGCATCCCA 137132
                                                                                                                                                                                                                                                                                                                                                                                               GlyThrGlyProGlySerLeuCysCysValGlnProArgAspLeuValProCysValPro 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgSerSerGlnGlnSerIleLysSerLeuAlaTrpArgProArgArgLysTrpPheCys 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGAAATTTCTAAGCAGCAAAACATTCAAGGTGTGACTTGGGTCCTGTTAAATGGATTC 136832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGluIleSerLysGlnGlnSerIleGlnGluValThrTrpValLeuLeuLysAlaPhe 133
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                                                                                                                                                                                                                    ArgIleGluValTrpGluProProIleArgPheGlnLysIleTyrGlyAsnProTrpMet 282
                                                                                                                                                                                                                                                                                                               ValAsnSerAlaValAlaSerGluGly-----
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DOE Joint Genome Institute
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Quality: Phrap Quality >=40 99.8% of Sequence;
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GlyGlnPhePheProPheGlyThrAlaValPheThrGlnCysLeuTyrLeuHisCys
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAGGCAGAAGTTTGCTGCAGGGGCAGGGCCTTCATGGAGAACCTCTGCTAGGGCAGTG 54860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuArgPheAspCysProThrGlyPheArgThrTyrMetGlyProValProLeuCysPhe 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuHisCysHisAspLeuAspValArgHisGlyValLysArgAspHisPheGlyAla 402
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Homo sapiens chromosome 5 clone
SEQUENCE, 36 unordered pieces.
ACO44889
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoc;
                                                                                                          Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                  Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 188749 bases at least Q40 Consensus quality: 180047 bases at least Q30 Consensus quality: 184014 bases at least Q20 Insert size: 190000; agarose-fp Insert size: 196268; sum-of-contigs Quality coverage: 3.8 in Q20 bases; sum-of-contil
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                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 36 contlys. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 792_C_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT
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1015: contig of 1015 bp in length 1115: gap of 100 bp
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3 7012: gap of 3 8145: contid of

2284: 2384: gap 3898:

contig of contig

3998:

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gap of

5359:

0562 20661:

14: gap of 18527: cont

30120:

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83452 83551: gap of 100 bp 83552 92170: contig of 8619 bp in len 92171 92270: gap of 100 bp 92271 96333: contig of 4063 bp in len 96334 96433: gap of 100 bp 96434 103218: contig of 6785 bp in len 103219 103318: gap of 100 bp 112554 112553: contig of 9235 bp in len 112554 112653: gap of 100 bp 112654 112339: contig of 10586 bp in len 123240 123339: gap of 100 bp 112654 12339: gap of 100 bp 112654 133922: sontig of 14582 bp in len 137922: 139013: contig of 19892 bp in len 137921: gap of 100 bp 138022: 159013: contig of 19892 bp in len 157914 158013: gap of 100 bp 158014 189768: contig of 19852 bp in len 159014 158013: gap of 100 bp 158014 158014 158013: gap of 100 bp 158014 158014 158014 158014 158014 158
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18084: contig of 4512 bp 1
85 38184: gap of 100 bp
15 41069: contig of 2885 bp ir.
100 bp
1100: gap of 100 bp
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35 25287: contig of 2703 bp

38 25387: gap of 100 bp

38 27603: contig of 2216 bp

30 2703: gap of 100 bp

30 2703: contig of 2317 bp
     /organism="Homo sapiens"
/db_xref="taxon:9606"
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79286: contig of 6496 k
79386: gap of 100 bp
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67628: contig of 6546 k
67728: gap of 100 bp
72690: contig of 4962 k
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18527: contig of 1313 bp
18627: gap of 100 bp
20561: contig of 1934 bp
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17114: contig of 2098 bp in
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22484: contig of 1823 bp in
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33472: contig of 3352 b
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2690: contig of 4962 bp
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243 AlaSerProLysProTrpGlnLeuProSerGlyValGluProValGlyAlaLysLysSer
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18628. .20561
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/clone_lib="RPCI-11 Human Male
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/map="5"
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5 M
                             Submitted (14-MAR-2002) Genome University School of Medicine,
                                                                                                                           Direct Submission
Submitted (13-JAN-2002) Genome
University School of Medicine,
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Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                               4 (bases 1 to 91323) Waterston, R.H.
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The sequence of Homo sapiens BAC
                                                                 Direct Submission
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                             Sequencing Center, Washington 4444 Forest Park Parkway, St.
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                                                                                                                                                                           Submitted (03-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 21, 2002 this sequence version replaced gi:19424673.
                                                                                                                                                                                                                                                                                                                              Waterston,R.H.
Direct Submission
Submitted (21-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                          Direct Submission
Submitted (03-APR-2002)
                                                                                                                                                                                                                                                                                  6 (bases 1 to 91323) Waterston, R.
                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH1178E06
                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                      ----- Genome Center
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.choriorg The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa K., Woon, P.Y., Zhao, B., Frenq Tateno, M., Catanese, J. J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome VECTOR: pBACe3 Frengen,E one male Jong

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-507C18,
the clone sequenced to the right is RP11-259120, 2000 bp overlap; 2000 bp overlap.

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                                                                            /rpt_family="Alu"
436. .589
                                                   /rpt_family="L1"
752. .821
                                                                                                                                              /clone="RP11-1178E6"
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126. .435
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                                  nArgSerSerGlnGlnSerIleLysSerLeuAlaTrpArgProArgArg---LysTrpPh 212
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                                                                          23474. .23000
/rpt_family="MaLR"
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rpt\_family="Alu"

family="L1"

\_family="MER1\_type"

family-"MIR"

.family="(CA)n"

family-"Alu"

family-"MIR"

family-"AT\_rich"

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family="(TA)n"

family-"ERVK"

family-"ERV1"

\_family="L1"

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ly-"MaLR"

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18659

family-"MER1\_type"

family-"MIR"

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Group. Fur http://www.
                                                                                                                    regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                               requests: clonerequest@sanger.ac.uk
On Oct 26, 2001 this sequence version replaced gi:15020340.
During sequence assembly data is compared from overlapping clones
                                                                                                     database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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    Further information can be found at www.sanger.ac.uk/HGP/Chr1
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US-09-997-610-2_COPY_18_459 (1-442) x AL139216 (1-112515)
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                                                                                                                                                                                                              182 GlnAspAsnGlyGluAsnIleSerTrpThrCysGlnArgSerSerGlnGlnSerIleLys
                                                                                                                                                                                                                                                                                                                                                                                 142 LysSerSerGluAsnLeuHisProAspAsnValIIeLysLysLysAsnProPheSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 IleGlnGluValThrTrpValLeuLeuLysAlaPheSerPheIleArgGluAlaGluHis 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPheAlaCys
                        CysCysValGlnProArgAspLeuValProCysValProValAsnSerAlaVal-----
                                                                                   TCACAAGCCTGGAGGCCTAGGAGGTGAATGTGGTTTTGTGGGCTGGGCCCAGGGTCCCGG
                                                                                                                                                                                                                                                                                        GlyLysPheLysLeuAlaAlaGluIleCysIleCysAsnGluGluLeuAsnValAsnPro
TGTTGTGTGCAGTCTAGGTATTTTGTGCCCTTGCATCCCAGCCACTCCAGCCGTGACTAAA
                                                                                                          SerLeuAlaTrpArgProArgArg---LysTrpPheCysGlyThrGlyProGlySerLeu
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/db_xref="taxon:9606"
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                                                                This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                      Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 19, 1997 this sequence version replaced gi:1772951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from clone RP3-345P10 on chromosome 22 Contains a pseudogene similar to 14-3-3 protein theta-subtype, parts of 2 novel genes based on ESTs, a testis-specific mRNA, ESTs, STSs and
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 137785)
  This sequence was generated from human chromosome 22, constructed
                                                                                                                                                                                                                                                                                                                  Whiteley, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP3-345P10 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between neighbouring submissions. The start of this sequence overlaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping Group. Further information can be found http://www.sanger.ac.uk/HGP/Chr22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones
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                                                                                                                                                                                                                                         /note="HAL1 repeat: ma
9549. .10178
/note="MER92B repeat:
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/note="L1ME
1936. .2241
                                                                                                                                 /note="LIMCb repeat: matches 196. 13084. .13197
                                                                                                                                                                                                                                                                                                               9137. .9384
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                                                14078.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="dJ345P10.4 (testis-specific mRNA)"
/note="match: ESTs: Em:AF012350 Em:AF012385"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Join(<7248. .7402,16817. .>16920)
/gene="dJ345P10.4"
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/db_xref="taxon:9606"
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                    /note="MLT1D repeat: matches 1.
                                                                                                                                                                                                  note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                 /note="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="22"
                                                                'note="MER5A repeat:
                                                                                                               note="AluJo/FRAM repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="dJ345P10.4"
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repeat: matches

27.

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/note="HAL1 repeat: matches 155. .499 of consensus"
15448. .15632
                /note="MIR repeat: matches 13. 35858. .35926
                                                     /note="L1MB3 repeat: matches 6028. .6181 of
33191. .33417
                                                                                                                                                                                             /gene="dJ345P10.2"
/note="match: GSS: Em:AQ138484"
complement(31307...31543)
/gene="dJ345P10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2583. .2709 of consensus" complement(join(26812. .27006,35225. .35343,42569./gene="dJ345p10.2"
                                                                                                                                                                                                                                                                                                       /note="AluY repeat: matches 1. 30575. .30981
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/product="dJ345P10.2 (part of a novel gene)"
/protein_id="CAB63029.1"
/db_xref="GI:6572210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<26812. .27006,35225./gene="dJ345P10.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2527. .2710 of 17821. .17886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HAL1 repeat: matches 1094.
15772. .15873
                                                                                                                                       /note="match: GSS: Em:AQ269272"
31874 . .32097
/note="LTR8 repeat: matches 1.
                                                                                                                                                                                                                                                                    /note="MSTA repeat: matches 1.
complement(31305. .31756)
                                                                                                                                                                                                                                                                                                                                                                                             /translation-"PKQKVADSELACEQAHQYLVTKAKNRWSDLSKNFLETDNEGNGI
LRRDIKNALYGFDIPLTPREFEKLWARYDTEGKGHITYQEFLQKLGINYSPAVHRPC
ADDYFNEWGHTTKPQQLQEEMKELQQSTEKAVAA"
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21079, .24772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluSg repeat: matches 1.
19712. .20092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluY repeat:
15997. .16043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="HAL1 repeat: matches 1431. .1533 of consensus"
15878. .15988
                                                                                                    'note="AluSc repeat: matches 1. .291 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match: ESTs: Em:AA497915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alusx repeat: matches 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L1MA5 repeat: matches 6128. .6295 of consensus"
26004. .26282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluJb repeat: matches 1. .309 of consensus"
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20737. .21046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSx repeat: matches 1 .309 of 17306 .17475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="12 copies 2 mer aa 95 conserved"
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16044. .16067
                                                                                                                                                                                                                                                                                                                                                             'note="MER5A repeat: matches 9. .93 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MA4 repeat: matches 5810. .6286 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1MA4 repeat: matches 2179. .5810 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="3 copies 20 mer 85 conserved"
                                                                                                                       .32395
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 repeat:
 matches 157.
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                                   .249 of consensus"
                                                                                                                                           . 227
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                                                                                                                                                                                                                                                                                 GlnGlnSerIleGlnGluValThrTrpValLeuLeuLysAlaPheSerPheIleArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTGGAACTTTGAACTTGAGAGAGATGATTTAGGGTATCTGGCAGAAGAAATTTCTAGG
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:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACATTTTAGCAAAAAGACTGGCAGCATTTTGCCTC---
 GGGTCCCTGAGCTGTGCAGACTAGGGACTTGGTGCCCTGCATCCCAGCAGCTCCAGCC
                             GlySerLeuCysCysValGlnProArgAspLeuValProCysValProValAsnSer---
                                                                    CCCCTCCCATCACAGGCCTGGAGGTCTAGGAGGAAAAAGCAGTTTCATAGGCTGGGCCCA
                                                                                         SerIleLysSerLeuAlaTrpArgProArgArg---LysTrpPheCysGlyThrGlyPro
                                                                                                                                         ATTAATCCCCAAGACAATGGTGAAAATGTCTCCAGGGCATGTCAGAGGTCTTCACAGCAG
                                                                                                                                                                                                                TTTTCTGAGCAGAAATTCAAGCTGGTGGCAGAAATGTGCATAAGTAACGAGGAGGAGAAT
                                                                                                                                                                                                                                                PheSerGluGlyLysPheLysLeuAlaAlaGluIleCysIleCysAsnGluGluLeuAsn
                                                                                                                                                                                                                                                                                                                                                             CAGCAAAGCATTCAAGAGGTGACTTGGGTGATGTTAAAAGCATTCAGTTTTATGAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgValProGlyAsnTyrTyrSerSerPheAspValGluLeuHisHisCysLysValAsn 101
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/note="L1M4 repeat: matches 3997.
36680. .36998
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39353. .39666
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7761. .37882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1ME repeat: matches 4886.
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Matches:
Conservative:
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Indels:
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ORGANISM
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TITLE
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                                                    -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                               Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Jo: Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On Jun 21, 2000 this sequence version replaced gi:7689877.
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168080)
DOE Joint Genome Institute.
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                               site: http://www.jgi.doe.gov
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Consensus quality: 140999 bases at least Q40
Consensus quality: 155370 bases at least Q30
Consensus quality: 158861 bases at least Q20
Consensus quality: 158861 bases at least Q20
Estimated insert size: 161080; agarose-fp estimation
Estimated insert size: 164480; sum-of-contigs estimation
Quality coverage: 3.7 in Q20 bases; agarose-fp estimation
Quality coverage: 3.62 in Q20 bases; agarose-fp estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
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Center clone name: RPCI-11_204G18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.  
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                                                                                                                                                                                                                                                                                                          LysLysLysAsnProPheSerGluGlyLysPheLysLeuAlaAlaGluIleCysIleCys 173
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-204G18"
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5: contig of 7076 bp in length
6: gap of unknown length
7: contig of 9732 bp in length
7: gap of unknown length
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8: contig of 14541 bp in length
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9: contig of 24102 bp in length
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Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 199579)
DOE Joint Genome Institute.
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AC093536.2 GI:21717113
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Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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                                                                                      Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 9, 2002 this sequence version replaced gi:16259134.
                                                                                                                                                                                                     Submitted (04-OCT-1999) Genome University School of Medicine,
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Center project name: H_NH0374C05
                Contact: sapiens@watson.wustl.edu
                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
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(1998)
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                                                                                                                                                                                                     Sequencing Center, Washington 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                            RP11-374C5
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                                                                                                                                                                                                        Louis,
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NOTICE: This sequence may not represent the entire insert It may be shorter because we only sequence overlapp overlapping of this

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-318F5, 2000 bp overlap; clone sequenced to the right is RP11-299014, 2000 bp overlap. Actual start of this clone is at base position 153702 of RP11-318F5; actual end is at base position 4782 of RP11-299014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The Clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone sections once, or longer because we between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphisms have been identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://bacpac.med.buffalo.edu)
/ECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from AC016715 was used to finish this clone, AC011238
                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Mus musculus (NID:g12576746) uu72f01.x1" 628. .833
                                                                                                                                                                                                                         /note="match to 645. .1151
                                                                                                                                                                                                                                                                                                                       628
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374. .400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11" 195. .589
                                                                            /note="match to EST 1593. .1870
                                                                                                                              /note="match to 1108. .1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                /rpt_family="Alu"
1665. .1667
                                                                                                                                                                             /note="match to EST BE466172 (NID:g9511947) hz60c11.x1"
788. .821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
    'note="match to EST AA625701 (NID:g2538088) zu86c07.s1"
                                                                                                                                                                                                                                                                                         note="match to EST AA328123 (NID:g1980388)"
                                                                                                                                                                                                                                                                                                                                           /note="similar to Rattus norvegicus EST BI289336
(NID:g14946795)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST BE856700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match to EST AW952412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note='
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-374C5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 match to EST AA443394
                                                                                                                                                    EST
                                                                                                                                                                                                                                               EST AI471723
                                                                                                R51616 (NID:g813518) yg77b04.s1"
                                                                                                                                               N39733 (NID:g1163278) yx92g01.r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between AC016715 and AC011238
                                                                                                                                                                                                                                          (NID:g4333813) tal6a05.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NID:g10369992)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NID: g8142094)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NID:g2156069) zw87b01.r1"
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/note="similar to Rattus norvegicus EST BI289336

(NID:g14946795)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
5865. .6033
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NOte="similar to Rattus norvegicus EST AI058342
(NID:g3332119)"
                                                                                                                         /note="match to EST 11112. .11425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4046.
                                                   /note="match to EST
                                                                                                                                                                        /note="match to EST
11112. .11453
                                                                                                                                                                                                                    note="match to EST 10973. .11380
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(NID:g12576746) uu72f01.x1"
note="match to EST N26638 (NID:g1140986) yx92g01.s1"
                                                                          note="match to EST"
| 1117. .11142
                                                                                                                                                                                                                                                                                                                                                                 rpt_family="MIR"
10562. .10656
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                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="Alu"
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                                                                                                                                                                                                                                                                                            family-"Alu"
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                                                 AA443394 (NID:g2156069) zw87b01.rl"
                                                                                             N39733 (NID:g1163278) yx92g01.rl"
                                                                                                                                                                                                                                          AV725468 (NID:g10830886)"
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                                                                                                                                               BE856700 (NID:g10369992)"
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Percent Similarity:
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Query Match:
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                                                                                              PheSerPheIleArgGluAlaGluHisLysSerSerGluAsnLeuHisProAspAsnVal
                                         GCAGTGCAGAAGGGAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCTACTGGGGCACC
                                                                                                                                                     sGlnArgSerSerGlnGlnSerIleLysSerLeuAlaTrpArgProArgArgLys---Tr
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oSerSerArgAlaValArgArgSerProProSerSerArgLeuGlnLysGlyArgSerTh
                                                      gValValGlnLysGlyAsnValGlyTrpGluProProHisArgValProSerGlyAlaPr
                                                                                                                                                                                                                                                                      CATCCCAGCTGCTCCAGCCACGGCTGAAAGGGGCCCAATGTAGAGCTCAGACTGTGGCTTC
                                                                                                                                                                                                                                                                                                  sValProValAsnSerAla------ValAlaSe
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                                                                                                                                                                                                               AGAGGATGCAAGCCTCAAGACTTGGCAGCTTCCACGTGGTGTTGGGCCTGTGAGTGCATA
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11654.
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/note="match to EST
11581. .11621
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12696. .13327
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11795. .12448
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                                                        Sequencing vector: M13; 80%
Sequencing vector: plasmid; 20%
Sequencing vector: plasmid; 20%
Chemistry: Dye-primer ET; 80% of reads
Chemistry: Dye-terminator Big Dye; 20% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181767 bases at least Q40
Consensus quality: 181800 bases at least Q30
Consensus quality: 185054 bases at least Q20
Insert size: 195000; agarose-fp
Ouality coverage: 5.73 in Q20 bases; agarose-fp
Quality coverage: 5.24 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aAlaGlyMetGluSerValProTyrLysThrValValAlaGluLeuThrLysThrValGl
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                                                                                                                                                                                                                                                                           Center project name: H_NH0311D08
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 19, 2000 this sequence version replaced gi:8569912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG;
                                                                                                                                                                                                                                                                                                                              Center: Washington University
Center code: WUGSC
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Direct Submission
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                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Homo sapiens
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Mammalia; Eutheria;
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NOTE: This is a 'working draft' sequence. It currenconsists of 9 contigs. The true order of the pieces is not known and their order in this sequence record
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RP11-311D8,
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DRAFT SEQUENCE,
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Percent Similarity:
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Pred. No.:
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                                              121670 --- GAAGAAATGTCTAAACAGCAAAGCATTCAAGAGGTGACTTGGATGCTGTTGAGGGCA
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                                                                        LysGluGluIleSerLysGlnGlnSerIleGlnGluValThrTrpValLeuLeuLysAla
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                                                                                                                                CysLysValAsnIleTrpLeuMetArgLysGlnIle------
               PheSerPheIleArgGluAlaGluHisLysSerSerGluAsnLeuHisProAspAsnVal
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59731. .94082
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29935. .39165
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/chromosome="2"
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3: contig of 2035 bp in length
0: gap of unknown length
2: contig of 34352 bp in length
2: contig of 34352 bp in length
2: gap of unknown length
0: contig of 44618 bp in length
0: gap of unknown length
0: gap of unknown length
0: contig of 48998 bp in length
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AUTHORS
TITLE
                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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Score:
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                                                                                                                                                                                                                                                                                                                  source
   86
 CysLysValAsnIleTrp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 91914 bases at least Q40
Consensus quality: 97497 bases at least Q20
Consensus quality: 98217 bases at least Q20
Consensus quality: 98217 bases at least Q20
Estimated insert size: 100000; pulse field gel estimation
Estimated insert size: 98884; sum-of-contigs estimation
Quality coverage: 6.94 in Q20 bases; pulse field gel estimation
Quality coverage: 6.94 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* to the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 2, 2000 this sequence version replaced gi:7711894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Project Name: 673152
Center clone name: CITB-H1_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Joint Genome Institute Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 10816: contig of 10816 bp in length
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Joint Genome Institute
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                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2118M3"
/clone_lib="CalTech human
a 18796 c 20008 g 30497
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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14198: contig of 3282 bp in length
14298: gap of unknown length
47746: contig of 33448 bp in length
47846: gap of unknown length
80349: contig of 32503 bp in length
80349: gap of unknown length
95940: contig of 15491 bp in length
96040: gap of unknown length
99084: contig of 3044 bp in length
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                                                                                CCATTAAGATTTTACTGCCCTGCTGGATTTTGGACTTGCATCAGGCCTGTAGCCCTTTGT
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                                                                                                                     AlaLeuArgPheAspCysProThrGlyPheArgThrTyrMetGlyProValProLeuCys
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                                                                                                                         GAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTGGGGGTGCTGTTAAAGGTATTCAGT
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                           LysLysAsnProPheSerGluGlyLysPheLysLeuAlaAlaGluIleCysIleCysAsn 174
                                                          TTTATAAGGGAAACAGAGCATAAAATCTCAGAAAATTTCCAGCCTGATAATGCAATAGAA
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Submitted (15-AGG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 15, 2001 this sequence version replaced gi:12331465.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (22-CAN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 133790)
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Direct Submission
Submitted (15-5EP-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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Quality: Phrap Quality >=40 99.6% of Sequence;
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                                                                                                                                                                            CAACTCTTGCATCAGTGTGATCTGGATTTGAGACATGGAGTCAAAGGAGATCATTTTGGA
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                                                          TTTGGCCAATTTCTCCCATTTGGAATGGCTGTATTTACCCAAGGCCTGTACCCACATTGT
                                                                                                                     CCATTAAGATTTTACTGCCCTGCTGGATTTTGGACTTGCATCAGGCCTGTAGCCCTTTGT
                                                                                                                                                AlaLeuArgPheAspCysProThrGlyPheArgThrTyrMetGlyProValProLeuCys 421
                                                                                                                                                                                                                                      AGGAGGAGACTGTACCCTGCAAAGCCACAGAGGCAGAGCTACCCAAGACCATGGGAACC
                                                                                                                                                                                                                                                          GlyMetGluSerValProTyrLysThrValValAlaGluLeuThrLysThrValGlyIle 381
                                                                                                                                                                                                                                                                                                     AGCTTGCACCATGTGCCTGGAAAAGCCACAGACACTCAATGCCAGCCTGTGAAGGCAGCC
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-O-/cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23843/app_query.fasta_1.1635
-O-/cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23843/app_query.fasta_1.1635
-DE-EST _OPMT-fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-2000000000
-USER-US0997610_eCGN_1_1_1871_erunat_10022003_160823_23843 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPDENT-0.5 -FGAPOP-6 -FGAPEXT-7
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seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed,

## SUMMARIES

Result No.	t . score	% Query Match	Length	DB	ID	Description
;	1 92	6.	372	10	77	772103
	2 88	54.3	447	9 !	93	284
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	œ	4	531	9	934	34261 SWOVL3CA
	80	ω.	399	10	E5 (	588347
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O	. 80	w	501	و	AA847768	47768 oe99f07.
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	2 5	۸,	609		AW675980	AW675980 SWYD25CAU
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1	œ	2	563	10	AW348031	48031
1	8	2	570	10	AW347952	AW347952 SWYD25CAU
, <u>, , ,</u>		۰,	571	10	AW225414	225414
,	<b>.</b>	0,	500	- -	AW675844	AW675844 SWYD25CAU
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4	8		726	14	7134	BQ771348 UI-M-F10-
4	8	1.	738	12	6433	64336

## ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BB772103 LOCUS DEFINITION REFERENCE EST

BB772103 RIKEN full-length enriched, B16 F107 cells Mus musculus cDNA clone G370139P03 3', mRNA sequence.

BB772103 BB772103

вв772103.1 GI:16213794

house mouse.

Mus musculus Eukaryota; Mammalia; | ikaryota; Metazoa; ammalia; Eutheria; (bases 1 to 372) Chordata; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Mus.

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,

AUTHORS

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BASE COUNT
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y. and Hayashizaki,Y.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370139P03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pooled tissues ; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
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KEYWORDS
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1 AlaGlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGly
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L., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,T., Martin,J.,
Steptoe,M., Theising,B., White,Y., Wylie,T., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Underwood,K. and Marra,M.
Molecular Parasitology OvL3
Unpublished (1998)
Contact: Steven A. Williams
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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//note="Vector: lambda UniZap XR; Site_1: Ecor I; Site_2:
//note="Vector: lambda UniZap XR; Site_1: Ecor I; Site_2:
//note="Vector: lambda UniZap XR; Site_1: Ecor I; Site_2:
Xho I; Cutaneous filarial nematode parasite of humans.

mRNA was prepared from third stage infective larvae of
Onchocerca volvulus isolated from mosquitoes 10 days after
infection and converted to double stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNAse H
and DNApol I. The library had 1.8 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Wenhong Lu. The library is
available from Dr. S.A. Williams, email genome@smith.edu."
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High quality sequence stop: 456.
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Unpublished (1998)
Contact: Steven A. Williams
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/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
Xho I; Cutaneous filarial nematode parasite of humans.
MRNA was prepared from third stage infective larvae of
Onchocerca volvulus isolated from mosquitoes 10 days after
infection and converted to double stranded cDNA using
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/db_xref="taxon:6282"
/clone="onch318"
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Unpublished (1998)
Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome@smith.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4135853826
                                                                                                                                                                                                 /note-"vector: lambda Unizap xR; Site_1: EcoR I; Site_2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu." a 130 c 139 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sierra Leone"
/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Onchocerca volvulus infective larva cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="onch596"
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                          LeuProGlnTyrThrGly 26
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194129 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BE588347.1 GI:9841386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and _minmatch 12 options.
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BACKWARD: GTTTTCCCAGTCACGACG
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Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lb="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disestates."
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US-09-997-610-2_COPY_18_45 (1-28) x AA857968 (1-445)
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorthum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1407
Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 284.
BE483103 499 bp mRNA linear 169146 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. BE483103 BE483103.1 GI:9602636
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="NCI_CGAP_Pr25"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
   Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
1 (bases 1 to 501)
NCI-CGAP http://www.ncbi.nlm.n
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AA847768.1
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                 Homo sapiens
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Fax: 301 504 8414
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                                                                                    human.
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http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
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/lab_host="DH10B"
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Insert Length: 1068 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 339.
űnpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                          232389 BARC
BE846038
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Unpublished (1997)
Contact: Robert Strausberg,
                                                                   Mapping of Expressed gland cDNA library
                                                                                                     Wells, K.D
                                                                                                                   1 (bases 1 to 524)
Sonstegard, T.S., Ca
                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
                                                                                                                                                                                                          Bos taurus
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
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/note="Organ: colon; Vector: BluescribtsK-; Site
: Site_2: XhoI; Cloned unidirectionally. Primer:
dT. Pooled colon tumors. 5' adaptor sequence: 5'
dANTICGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTT" 3' Average insert size:
a 126 c 186 g 98 t
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/clone="IMAGE:1419781"
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                                                                                     Sequence
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                                                                                Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
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                                Single pass sequencing
                                                                                                                                                             Contact: Yoshikazu Sugimoto
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                                                   Email: kazusugi@cocoa.ocn.ne.jp
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                                                                                                                                                                                                                                                                      and Sugimoto, Y.
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              clone was obtained from a polyA-deleted cDNA library.
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and c
states."
Location/Qualifiers
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/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
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/lab_host="DH10B"
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Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                         Tel: 4135853826
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Department of Biological Sciences, Clark
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                                                                                                                                                                                                                                                                                                                      Email: genome@smith.edu
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/clone="E12A030C06"
/clone_lib="Bos taurus ca
/tissue_type="cantilage"
/dev_stage="fetus"
/dev_stage="young adult, twenty five days after infection"
/lab_host="XLI-Blue MRR'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from young adult worms isolated from
the peritoneal cavity of jirds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNAse H and DNA
pol I. The library has 6.2 x 105 independent recombinants
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was deleted from a Not1 site"
170 c 171 g 113 t
                                                                                                                                                                    /clone="SWYD25CAU08D04"
/clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BMYD25)"
                                                                                                                                                                                                                             /organism="Brugia malayi"
/db_xref="taxon:6279"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                               Seq
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Eukaryota; Metazoa; Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                 /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte-Waniewski. The
                                 library is available from Dr. S.A. Williams, genome@neal.smith.edu."
                                                                                                                                                                                                                                                                                                                    /organism="Brugia malayi"
/db_xref="taxon:6279"
/clone="SWYD25CAU13F09"
                                                                                                                                                                                                                                           /dev_stage="young adult, twenty five days after infection"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                 /clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmYD25)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                            transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email:
                                                                                                                                                                                                                                                   /dev_stage="young adult, twenty five days after infection"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.
Xho I; Lymphatic filarial nematode parasite of form young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brugia malayi"
/db_xref="taxon:6279"
                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmYD25)"
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SW31CA178SK Brugia malayi infective larva cDNA (SAW94WL-BmL3)
Brugia malayi cDNA clone SW31CA178 5' similar to cuticular collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blaxter,M.L., Raghávan,N., Ghosh,I., Guiliano,D., Lu,W., Willi, S.A., Slatko,B. and Scott,A.L. Genes expressed in Brugia malayi infective third stage larvae Mol. Biochem. Parasitol. 77 (1), 77-93 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome@smith.edu
                                                                                                                                                                                                                                                                                                          note="Vector: lambda Unizap XR; Site_1: EcoR I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. The internal parasite of humans mRNA was prepared from third stage infective larvae of Brugia malayi isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNASSE H and DNApol I. The library had 1.6 x 10E6 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                                                                         The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu. 106 c 119 g 60 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brugia malayi"
/strain="TRS Labs"
/db_xref="taxon:6279"
/clone="SW3ICA178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Brugia malayi infective larva cDNA
(SAW94WL-BmL3)"
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RESULT 15
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GCCGGACCACCTGGCAGACCAGGAAATAGTGGCAATGCTGGTCCACCAGGACCCGTGGGA 65
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Molecular Parasitology
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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//lab_host="E. coli XL1-Blue MRF/"
//lab_host="E. coli XL1-Blu
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585-3826 fax +1 413 585-3786
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/clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9)"
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Command line parameters:

MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23819/app_query.fasta_1.1635
-Q-/cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23819/app_query.fasta_1.1635
-DB-GenEmbl -QFMT-fastap -SUFFIX=-yge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=bto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER-US0997610_eCGN_11_3965_@runat_10022003_160823_23819 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: gb_ba:
2: gb_htg
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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30: em_htg_hum:*
31: em_htg_inv:*
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35: em_htg_rad:*
36: em_htg_wam:*
37: em_htg_wam:*
38: em_sy:*
40: em_htgo_num:*
41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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ALIGNMENTS

RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/HGP/Chr22 RP1-302D9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on Dec 13, 1999 this sequence version replaced gi:3164067. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission that the compared with a compared with search and the sequence of the compared with the compared with the sequence submission and the sequence submission that the compared with th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSSs,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z82198
Z82198.2 GI:6572207
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                        /note="AluSx repeat:
572. .759
/note="AluSq repeat: matches 2.
3323. .3343
/note="MLT1E repeat: matches 110
                                                                            2684.
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/note="Alusp repeat: matches 1.

1450. .1583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                    1687
                                                                                                                                                                                    /note="MIR repeat: matches
                                                                                                                                                                                                                                                                               /note="MER5A repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP1-302D9"
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TTA-282F2 is at 69682 in this sequence. The true right
TTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                    .1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _lib="RPCI-1"
                                                                                                                                            repeat: matches 2593.
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                                                                                               matches 3.
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/note="THE1B repeat:
4279. .4485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 147. 9110. .9280
                                                                                            14368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: 10784. .11201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: 10718. .11310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS:
complement(10249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(10204.
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/note="match: GSS:
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                                                                                                                                       /note="MIR repeat:
14061. .14367
                                                                                                                                                                                                                                  /note="MIR repeat: matches 76.
13806. .13919
                                                                                                                                                                                                                                                                               13699.
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13331. .13397
                                                                                                                                                                                       13945.
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/note="FAM 1
                                                                                                                                                                                                       'note="MIR repeat: matches 77.
                                                                                                                                                                                                                                                                                                    'note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                 'note="MIR repeat: matches 174.
                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2579.
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/note="MLTIE repeat: matches 359. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3653. .3928
/note="MLT1E repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="AluJb repeat: matches 9.
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                                          nık repeat: matches 141.
.14679
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10706)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      20513.
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                                                                                                                                                                                                                                                                                                                         /note="MER66-internal
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21882. .22254
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18713. .19133
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18324. .18392
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15728. .16027
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15669. .15727
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15304. .15399
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="33 copies 2 mer ta 68 conserved"
20513. .20666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="HERVFH21 repeat: matches 4657. .5784
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.5490. .15662
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Sequence 5
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Bell,M.P., Neff,T.B., Polarek,J.W.
Animal collagens and gelatins
Patent: WO 0134647-A 5 17-MAY-2001;
FIBROGEN, INC. (US)
                                                                                                                                                                                                                                                                                                                                         Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Bell,M.P., Neff,T.B., Polarek,J.W. and
Animal collagens and gelatins
Patent: WO 0134647-A 3 17-MAY-2001;
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Mammalia; Eutheria; Cetartiodactyla;
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University, 4444 Forest
6 (bases 1 to 68661)
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Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                             Submitted (22-AUG-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                        Submitted by:
                                                                                                                                                                   Submitted (29-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                        Waterston, K
                                                                                                                                                                                                                                                        University, Genome Sequencing Louis, MO 63110, USA
                                                                                                                                                                                                                                                                    Submitted (07-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                             Waterston, R.
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                          Department of Genetics, Washington University St. Louis , MO 63110, USA, and Sanger Centre, Hinxton Hail Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
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200 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTES:
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It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclose.

For a graphical representation of this cosmid sequence and its analysis see: http://www.wormbase.org/db/seq/sequence?name=Y51H7C;class=Sequence

## NEIGHBORING COSMID INFORMATION

we 5' cosmid is F54D12, 200 bp overlap; the 3' cosmid is H17B010 bp overlap.

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE\_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions, are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

LOCATION/Qualifiers

1. .68661

//organism="Caenorhabditis elegans"
//strain="Bristol N2"

rce 1...b8bb1
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1328. .1838.

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2368. .7728
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                            Score:
                                                                                                                                                                                   Alignment
                                                                                                                                                           Pred. No.:
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LYADTLFMFFEGVAEIIESNLPVLEHSYGLEKLLDFMFILQARIDEFFRRLHEEFDTR
RRLSHFNRLVDDVIHQKKAAEAVEDAPDPMEIDAIASEICMMNTSAEMYWRFVSRRIG
KNEVIRSPSGDGDDEENEEARQERHRLKEAKEQKMDQLLNRSRVGTKMQELIGNYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNYQTLLLLTSSEIARQIEQSLAKCQFNRYGALQLDREYRQICAYLTNVAGWSAREKV
GRLGQIVSLLNVETIDEAMEVWHNSKAMTSSATIRTLTLPEVRKVLALRADFPTVAIK
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LEHFYMLKSVQKAIKSDVKEDAGGLTSSIVDDVVFIIRKSIRRAAGSGNVDSVCATIN
NATALIDTVHGHLRQSIQGGVTSSNFASEAFTAYQQGKPVKEAADAQKQEQFLLAN
NSAKLSELLIELQKGLITEWAGVKRPDVEKNKLEHSTTQIEESAKKLASLAKHGVEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYADTLFMFFEGVAEIIESNLPVLEHSYGLEKLLDFMFILQARIDEFFRRLHEEFDTR
RRLSHFNRLVDDVIHQKKAAEAVEDAPDPMEIDAIASEICMMNTSAEMYWRFVSRRIG
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TASQHIHRFLTLDQAVFQIREFKQKDATDSIRHSYEVLSSAKERLSKILKSRLTESVQ
KGDVAEMQRFIKMFPLIHEPDEGLQRYSVFLNQKIDKLAEDNLAIMKAGGTDDNRRNV
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http://www.wormbase.org/db/seq/sequence?name=Y51H7C.6a;cla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEHFYMLKSVOKAIKSDVKEDAGGLTRCGDKKYRKRPLKQEKIC"
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yk400b1.3, yk400b1.5"
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/gene="Y51H7C.6"
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   1.08e+03
84.50
59.38%
50.00%
52.16%
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15048,5864. .6340,6802. .7129,7558. .7728)
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Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                        1 protein Y51H7C.9"
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1"
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SOURCE
ORGANISM
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US-09-997-610-2_COPY_18_45 (1-28) x AC006799 (1-278007)
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                                                                                   Query Match:
                                                                                                                                                                    Score:
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                                                                                                                                             Percent Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 278007)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Caehorhabditis elegans clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                 87340
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 66669)
   Miklos, G.L.,
An essential
                                                                           Molecular and mutational analysis of a gelsolin-family member encoded by the flightless I gene of Drosophila melanogaster Genetics 141 (3), 1049-1059 (1995)
                                                                                                                                                                                                                                                                                  Drosophila melanogaster tweety (tty), flightless (fli), dodo (dod penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds. AF01777 U80043 U28044
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Bell,M.P., Neff,T.B., Polarek,J.W. a
Animal collagens and gelatins
Patent: WO 0134647-A 11 17-MAY-2001;
                                                  8582612
                                                                                                                              Miklos, G.L.
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                                                                                                                                           Couet, H.G., Fong, K.S., Weeds, A.G.,
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/db_xref="taxon:9823"
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Yamamoto, M., Burns, R.G. and Maleszka, cell division gene of Drosophila, abs
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On or before Apr 2, 1998 this sequence version replaced g1:2098624,
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/gene="fli"
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/gene="tty"
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lesiGilgsypaaliivsligilfyLmytcorkprahsitslkyalsivtwccaa
igiGilygnodlhwgleptyladrydmytatroyhlitentitwnkirpolyeladif
dopvsnotalsklfvslnivognvtlatnaasdirrplmgismtheltrgdowelirw
pgtvatlalilvgvahrbsprollirgvcgpertroptgkiresonslnanasamatv
bctyspadbilystaprolptnyllhyfvgcpertroptgkiresonslnanasamatv
kkislyfkssgiopkigavnadlnsserlltottalvdckavhhnelaaargicegg
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PBELGHLKQKLEHLSLNHHRLEKIFGELTELSCLRSLDLRHHQLKNSGIPPELFHLEEL
TTLDLSHNKKEVPEGLERAKNLIVLMLSNNQIESTEPTEFIHLTDLLFLLSHNRLE
TLPPQTRRLINLKTLDLSHNPLELFQLRQLPSLQSLEVLKMSGTQRTLLNFPTSIDSL
                                                                                                                                                                                                                                                                                    /gene="fli"
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GPQIPAHOHPPSLHQQQQQPPPPSQQQQOLHQLKSPQQHQQQLQQHQQQQQQHHQQQ
HHQQQHQQQQQHHQQQQPNESDVVPISTAMDTAIYDRDKQIYKCSTLRQGGKFDPKY
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                                                                                                                        /product="flightless"
/protein_id="AAC28407.1"
/db_xref="GI:3004660"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Cantons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kasprzak, A., Mason, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66669)
                                                                                                                                                                                                                                                                                                                       .12023,12260. .12410,12533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Couet, H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayward, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                       .13783)
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/protein_id="AAC28408.1"
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GGGSAGGGDAPDEVHCLHLLVKHKGSRRPSSWREANITRTKEEAQLLLEVYRNKIVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVWIGSKACNEEAKLVQDIAEQMFNSPWYSLQILNEGDEPENFFWVALGGRKPYDTDA
EYMNYTRLFRCSNERGYYTVAEKCADFCQDDLADDDIMILDNGEHVFLWMGPRCSEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QOETRTDLAALEMPROSAMPLAEAEQLEEEWNYDLEMMEAFVLENKKFVRLPEEELGR
FYTGECYVELCRYCIPLEEEENOSEDGANPAADVSKSSANNQPEDEIQCYVYFWGGRN
AGNMGWLTFTETLDKKKFAMFGEELEVVRIFQOQENLKEMNSHFKRKFILHTGKRKKKA
HTAKGKSPVEFFHLRSNGGALTTRLIQINPDAVHLNSAFCYILHVPFETEDDSQSGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYGAT HLEPVAPA I TSLDPRHAFVLDLGTHI Y I WMGERSKNTLNSKARLMAEK I SKT
ERKNKCE I QLERQGEESAEFWQGLGMTS BEDADAEPP K RHY PEDY QPVQPRLYOVQLG
MGY LELPQVELPEQKLCHTLLNSKHVY I LDCYTDLFVWFGKKSTRLVRAAQYKLSREL
ENMMDRPDYALVMRYPEGNEMQ I FRTKFAGMDEVMAVDETRTAKSVAKTGANLTQWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                       PKAKEEEPAAPLVSGIEEAGMHIVLKKILKNDGKREGTPFSQQLLQNLSSDVLKAWLG
VNRACFVLLKLVEECPALLDDCKKAIAAERSLSQILADRKTPGAKLLAAKLDIGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(15308. .15493,15707. .16182,16281. .16683,
16752. .17454,18055. .18500))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(15247. .15493,15707. .16182,16281. .16683, 16752. .17454,18055. .18587))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNFLGARCRTVREEQGDESEQFLSLFETEVIYIEGGRTATGFYTIEEMIHITRLYLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGALKOLNLSCNRLITLPDAIHLLEGLDQLDLRNNPELVMPPKPSEASKATSLEFYNI
DFSLQTQLRLAGAAVPPSMPSSATPKDSTARKIRLRRGPRSEGDQDAAKVLKGMKDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(15247. .18587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {	t EATFDELARSYSDCSSAKRGGDLGKFGRGQMQAAFEDAAFKLNVNQLSGIVDSDSGLH}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(14131. .14252,14364. .14696,15066. .15603)
/gene="dod"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKLAYKSAQVYIQHMRIKQPERPRKLFLTMKNKESRRFTKCFHGWSAFKVYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNKIEEVVHGKFYEGDCYIVLKTKFDDLGLLDWEIFFWIGNEATLDKRACAAIHAVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDKDNEAGAVPEDGKPESLKPKRWDESLEKPQLDYSKFFEKDDGQLPGLTIWETENFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVALPAALCKLPKLRRLLVNDNKLNFEGIPSGIGKLGALEVFSAANNLLEMVPEGLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="pen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="pen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"dodo"
'product="small optic lobes"
'protein_id="AAC28409.1"
                                                                codon_start=1/
                                                                                                                                                                                                                     'product="small optic lobes"
                                                                                                                                                                                                                                                                                                                )oin(19098. .19602,20609. .21234,21502. .22414,22843. .23171.
23238. .24826,24899. .25405,25465. .25731,25803. .25945,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains pumilio repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="penguin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="dodo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(14195. .14252,14364. .14696,15066. .15175)
/gene="dod"
                                                                                                                                                                                           (19361.
                                                                                                                              .26181)
                                                                                                                                                        61. .19602,20609. .21234,21502. .22414,22843. .23171,
24826,24899. .25405,25465. .25731,25803. .25945,
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RESULT 8 AC013980

DEFINITION

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DB:

Score: Pred. No.:

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65849

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

COMMENT

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212172 by the submitte For further information on this sequence e-mail to fly@celer \* NOTE: This is a 'working draft' sequence.

\* This sequence will be replaced \* This sequence or will be replaced \* This sequence will be replaced \* This sequenc

to fly@celera.com the submitter.

accession number will be preserved

REFERENCE

AUTHORS TITLE JOURNAL

Adams, M. and Venter, J.C.

Direct Submission

mRNA

gene

CDS

mRNA

gene

CDS

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CDS

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US-09-997-610-2_COPY_18_45 (1-28) x AF017777 (1-66669)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCT 65851
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1 (bases 1 to 87089)
                                                                                                                                                   Drosophila melanogaster.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                        AC013980 87089 bp DNA linear HTG 16-NOV-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                 HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                            AC013980
AC013980.1 GI:6437355
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DAAAVGGGGGSAHQSGANEVKAPTALMLPLTSYALPMPMLQLFPSTAAGLRGSRSPSP
RMQLLPSLQOQRNSSSSGAIPKHSTGGSIYERNISTAGLANVHLQQGQGVGSASVSS
ASGGGSGAGAVGASTSSKKWQCPACTYDNCAASVVCDICSSPRGLASAVLGEALGRKS
VRVALTPADIRGESKLMENLRQLEETEALTKWQNIJGYGRDNSELFVDDSFPPAFKSL
YYNPATPADIRGESKLMENLRQLEETEALTKWQNIJGYGRDSELFVDDSFPPAFKSL
YYNPAGGAGEGNPVQWRRPBEINCUGGAYPWAVFRTPLPSDICQGVLGCWILLSAL
AVLAEREDLVKEYLVTKEIGGGGAYQVRLCKDGKWTTVLVDDLLPCDKRGHLVYSQAK
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SESESQVEEHSIYAKVWKGPKRATESKIMHDPGSSETLSGASAAAGTASAGIAAAQ
GAAAASRHDNKTYOLGNKSRKWMICIKCSYSVENRLWLGTCEMCEAKAEQOQQQLDLQQQ
QQQQQQQHHHHHHHHHLQQQQAEAPRDEPWTCKKCTLVNYSTAMACVVCGGSKLKSISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFSIAHRLTHRLANSRGLHDWGPPGATHCPPIENVHGLHAPRLIT*
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GLVVMVENRHENKWIHVKCDCQESYNVVSTRGELKTVDSVPPLQRQVIIVLTQLEGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLKLRNPWGHYSWRGDWSDDSSLWTDDLRDALMPHGASEGVFWISFEDVLNYFDCIDI
CKVRSGWNEVRLQGTLQPLCSISCVLLTVLEPTEAEFTLFQEGQRNSEKSQRSQLDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKQLWVPLIEKAVAKIHGCYEALVSGRAIEGLATLTGAPCESIPLQASSLPMPSEDEL
DKDLIWAQLLSSRCVRFLMGASCGGGNMKVDEEEYQQKGLRPRHAYSVLDVKDIQGHR
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NNNSSSSSGSNKLYENECVALAQQQLRAAAAQAAQAAATAVAIASSPSAKAMAEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVIFRTRSPAAPETGRLVEHSKRQVRGEVGCHKMLERDIYLLVCLAFNHWHTGIEDPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Rolt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Besson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibeywan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome X, region 20B-20C
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                            64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
                                                                                                              Stapleton, M., Strong, R., Zaveri, J.S., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished 2 (bases 1
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HTG.
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Sequence submitted by
                                                                                     Submitted (12-JUL-2001) Berkeley Drosophila Genome Project, MS
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Ba. Butenhoff, C., Champe, M., Chavez, C., Chew, M.,
                                                                                                                                                                                                                                                                                                                                                                                      Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
HOlt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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DOE Joint Genome Institute.
Direct Submission
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DOE Joint Genome Institute.
Sequencing of Mouse
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SEQUENCE, 62
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Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Packeb,J.M., Park,S.,
Pfeliffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
                                                                                Unpublished
                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Location/Qualifiers
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Berkeley, CA 94720
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Estimated insert size: 220300; agarose-fp estimation
Estimated insert size: 250317; sum-of-contigs estimation
Quality coverage: 3.11 in Q20 bases; agarose-fp estimation
Quality coverage: 2.74 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 62 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Ephydroidea; Drosophilidae; Drosophila
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33 241592: gap of unknown length
33 256417: contig of 14825 bp in length
Location/Qualifiers
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PUBMED
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7295493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287
20196006
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Adams, M.D., Celniker, S.E., Gibbs, R.A.,
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                                                                                                                                                                 VATVICKLFMIYEFKLICMDPVVNFTSVEVFKSECLSITGANNSGKTTLLKVVVNETK
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                                                                                                                                                                                                                                    GFWVILLAYLMASLCRNPCYGFLWLCGINSIGLVCFSQFYRTHPESMLLEPTFMAMYT
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Percent Similarity:
Best Local Similarity:
Query Match:
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AUTHORS
TITLE
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RESULT 14
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Sequence
AR014097
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Cappello, J. and Ferrari, F.A.
High molecular weight collagen-like protein polymers
Patent: US 5773249-A 30 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                 Unknown
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/db_xref="FLYBASE:FBgn0031170"
complement(join(65188. .65380,65443. .66216,66361. .66537,66595. .66745,66950. .67802,67867. .68234,68300. .70124,70196. .70784,72001. .72212))
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/db_xref="FLYBASE:FBan0001718"
/db_xref="FLYBASE:FBgn0031170"
/translation="MAKVTNWDKFVLLLWKNWTLQWNHKWQMVIELVLPAIFSLLLVLVRTLVDTEQKGVRYYNEQNLTDLNLLQKNGGFSKFEFILCYSPVNPVLKKLVEEAWQS
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71 c 67 g
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/db_xref="GI:7295524"
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Sequence 62
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I06482
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Cappello,J., Ferrari,F.A. and CO7H15.
FUNCTIONAL RECOMBINANTLY PREPARED SYNTHETIC
Patent: WO 9005177-A 19 17-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional recombinantly prepared synthetic protein polymer Patent: US 6140072-A 62 31-OCT-2000;
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Ferrari, F.A. and Cappello, J
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Search completed: February 19, 2003, 23:10:55 Job time: 581.136 secs

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GenCore version 5.1.3 Compugen Ltd.

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-Q-/cgn2_1/USPTO_spool/US09997610/runat_10022003_160823_23843/app_query.fasta_1.1635
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-UNITS-bits -STAFT-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL
-OUTFWT-pto -NORM-ext -HEAPSIZE-500 -MIMLEN-0 -MAXLEN-200000000
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-WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Maximum Match 100%
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Maximum DB seg length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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#### ALIGNMENTS

EST 20-MAR-2002

RESULT 1
BM967732
LOCUS
DEFINITION KEYWORDS SOURCE ORGANISM ACCESSION VERSION BM967732
499 bp mRNA linear EST 20-MAR-200 LM24HW0134 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone LM-24-HW-011-34 (5'), mRNA sequence. CON ESTBos taurus вм967732.1 BM967732 GI:19561919

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
1 (bases 1 to 499)
Yoon,D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R.,

REFERENCE

AUTHORS

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BE757276.1
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Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Omockchun-dong, Suwon, 441-350, Korea
                                                                                        BE757276 520
211669 MARC 2BOV Bos taurus
                           Bos taurus
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    Eukaryota; Metazoa;
Mammalia; Eutheria;
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/dev_stage="24 months old"
/lab_host="XL1-BlueMRF'strain"
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/sex="six males mixed"
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Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                  HisHisCysLysValAsnIleTrpLeuMetArgLysGlnIle 109
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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PheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAla
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P.L., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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BACKWARD: GTTTCCCAGTCAGACG
Plate: 63 row: 6 column: 13
Seg primer: ATTTAGGTGACACTATAG.
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.s. Vector identified by cross_match with the -minscorr
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Fax: 402 762 4390
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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/lab_host="DH10B"
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/db_xref="taxon:9913"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-8856
Fax: 81-559-81-6855
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BJ068972 NIBB Mochii normalized Xenopus tailbud library Xenopus Laevis cDNA clone XL051f08 5', mRNA sequence.
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/dev_stage="stage 25"
/dev_stage="stage 25"
/note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwcop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "

Wellcome/CRC Institute). "
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/clone="XL051f08"
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Characterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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011D22 of
                                                                                                                    This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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      /Organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="011D22"
/clone_lib="A"
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                                                                                                                                                                                                                                                 Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp
                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                             Kohara, Y., Shin-i, T.,
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                                                                                                                                                                                                                                    81-559-81-6855
/sex="mixture of female and
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
                                                                                /strain="d-rR"
/db_xref="taxon:8090"
/clone="MF01FSA024E16"
                                                               /clone_lib="MF01FSA cDNA"
                                                                                                                                             /organism="Oryzias latipes
                                                                                                                                                                                        Location/Qualifiers
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Takeda's lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV593019 Ser taurus cartilage E1CA005A05 5', mRNA sequence.
                              Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                      Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
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                                                                                                                                                                            Contact: Yoshikazu Sugimoto
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BB318780 RIKEN full-length enriched, adult male corpora
היישליומפשוחם Mus musculus cDNA clone B230377C02 3', mRNA sequence.
                                                                 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horl,F., Ishi,Y., Ito,M., Kawal,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
D., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 11, 2000 this sequence version replaced gi:9025815.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 689)
                                                      Contact: Yoshihide Hayashizaki
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/lab_host="DH10B"
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed t
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) for
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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rel: 81-45-503-9222
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                                                                                                                                                                                                       modified pBluescript KS(+) after bulk excision
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/dev_stage="adult"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK018742 2462 bp mRNA linear HTC 19-JAN:
Mus musculus adult male kidney cDNA, RIKEN full-length enriched
library, clone:0610011L15:procollagen, type VIII, alpha 1, full
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19–44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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clone:0610011L15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                   /clone="0610011L15"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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/db_xref="MGD:MGI:1912859"
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                                                                cDNA library"
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BQ419957 662 bp mRNA linear EST 23-MA faal2c05.yl zebrafish fin day3 regeneration Danio rerio cDNA 5909744 5' similar to TR:Q9ZIK4 Q9ZIK4 COLLAGEN ALPHA 1 TYPE contains element MSR1 repetitive element; mRNA sequence.
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/db_xref="GI:12858613"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Stephen L. Jo
Washington University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="zebrafish fin day3 regeneration"
/sex="mixed male and female"
/tissue_type="3 day fin regenerates"
/lab_host="E. coli XLOLR"
/lab_host="E. coli XLOLR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; 1st
strand cDNA primed with (GA)IOACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5 adapter (5')
-aatteggacagg-3', 3'.gccgtgctc-5', cDNA was cloned
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                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogaba,Y., Suzuki,H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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AV243093
AV243093.2 GI:16386815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
On Nov 4, 1999 this sequence version replaced gi:6230520
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                         ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
Hayashizaki,Y.
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                                                                                                                Computer-based methods for the mouse full-length cDNA
                                                                                                                                              Y. and Hayashizaki,Y
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Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                         Shibata, K., Itoh, M.,
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                                                                                   PheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPheAla
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                                                                                                                                                                                                                                                                                               -----ProGlnTyrThrGlyGlu-----
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                                                    TTTGACAAGCTGCTCTACAACGGCAGACAGAACTACAATCCGCAGACAGGCATCTTCACC
                                                                                                                        ATGCCTGCGTTTACTGCCGAGCTGACTGTACCTTTCCCCACCGGTGGGGGCCCCAGTGAAG 364
                                                                                                                                                      ArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLysProIleIle
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further details.
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prepared and sequenced in Mouse Genome
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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921 bp mRNA linear EST 26-NOV-1997 ve40g07.rl Soares_mammary_gland_NbMNG Mus musculus cDNA clone IMAGE:820668 5' similar to gb:U37222 Mus musculus 30kDa adipocyte complement-related protein Acrp30 (MOUSE);, mRNA sequence. AA673154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:820668"
                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_mammary_gland_NbMMG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                     double-stranded cDNA was ligated to Eco RI rs (Pharmacia), digested with Not I and cloned into t I and Eco RI sites of the modified pT7T3 vector. ovided by Dr. Minoru Ko, Wayne State Univ. Library ucted and normalized by Bento Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    College: No. 1. Contact the Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

This_clone is available royalty-free through LLNL; contact the This_clone is available royalty-free through royalty-free through ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
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Contact: Robert Strausberg, Ph.D.
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468 bp mRNA linear EST 02-JUN-2000 ug08h07.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1531069 5' similar to gb:U37222 Mus musculus 30kDa adipocyte complement-related protein Acrp30 (MOUSE);, mRNA sequence.
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NCI-CGAP ncar Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
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/db_xref="taxon:10090"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uu19e06.yl Soares_mammary_gland_NMLMG Mus musculus cDNA cl
IMAGE:3372418 5' similar to gb:U37222 Mus musculus 30kDa a
complement-related protein Acrp30 (MOUSE);, mRNA sequence.
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Mammalia; Eutheria;
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             gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-Stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library
                                                                                                             /note="Vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
                                                                                                                                                   /tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                           /sex="female (lactating)"
                                                                                                                                                                                                         /clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                             /clone="IMAGE:3372418"
                                                                                                                                                                                                                                                 /organism="Mus musculus"
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RESULT 15
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,P., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayartsı,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                        RIKEN Mouse ESTs (Arakawa,T., et al.
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                          Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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US-09-997-610-2_COPY_18_149 (1-132) x BB625284 (1-633)
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                         ProCysProAspIleGluArgSerAlaPheThrValLysLeuSer-----GlyLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer \lceil 5' \rceil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector: a modified pBluescript KS(+) after bulk from Lambda FLC I. Cloning sites, 5' end: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="cecum"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, adult male cecum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="9130217G22
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Matches:
Conservative:
Mismatches:
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Qy 53 ProLeuProPheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeu 72	Sear Job	Db .	٥٧	Ф	Qy	망	Qy	망	Qy
ysProllellePheThrGlyValLeuTyrAsnAlaGlnArgAspLeu	ch con time :	562	111	502	93	442	73	382	53
2 41 01 10	pleted: February 19, 2003, 19:35:51 1032.49 secs	CACACCAAAGAA 573	AlaAsnLvsGlu 114	ATCACTGTGTTCTCCAAGAATGTGCAGGTATCTTTGGTCAAAAAACGGGGTAAAAGTCCTG	ValGluLeuHisHisCysLysValAsnIleTrpLeuMetArgLysGlnIleLeu 1	AATGTAGCGACGGGAAGTTCACCTGCCACGTGGCAGGTGTCTATTACTTTACCTACC	LysGluAlaMetGlyValPheAlaCysArgValProGlyAsnTyrTyrSerSerPheAsp 9	CCTCCCCCAGATGCACCCATTAAATTCGATAAGATCCTATACAATGAACTGAACCACTAC 4	ProLeuProPheLysProlleIlePheThrClyValLeuTyrAsnAlaGlnArgAspLeu 7
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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh

-Q-cgn2_1/USPT0_Spool/US09997610/runat_10022003_160823_23819/app_query,fasta_1.1635
-DB-GenEmb1 -QFMT-fastap -SUFFIX=rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXY-0

-UNITS-bits -STARP-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXIEN-2000000000

-USER-US09997610_@CGN_1_1_3955_@runat_10022003_160823_23819 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120

-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOXT-7

-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_rod:*
36: em_htg_vrt:*
36: em_htg_other:*
40: em_htgo_nus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

222 2322 24444 20011222 2422 2422	C C 114 C C 113 C C 114 C C 224 275 C 224 276 57	Result
	32 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	Score
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ALIGNMENTS

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AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Dec 13, 1999 this sequence version replaced gi:3164067. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission to the control of the overlapping clone name.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/Chr22
RP1-302D9 is from the library RPCI-1 constructed
Park Cancer Institute by the group of Pieter de J
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSSs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the entire insert end of clone CTA-282F2 is at 69682 end of clone CTA-415G2 is at 55167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z82198
Z82198.2 GI:6572207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VECTOR: pcypac2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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                                                    /note="AluSc repeat: 2684. .2981
                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1.
572. .759
                                                                                           2350
                                                                                                                                                                1450
                                                                                                                                                                                                                                                                                                           /note="MER3 repeat: matches 144.
246. .571
                                                                                                                                                                                                                                                                                                                                               188.
                                                                                                                                                                                                /note="MER5A repeat: matches 26.
1033. .1336
                    /note="Alusq repeat: matches 2.
3323. .3343
                                                                                                                                                                        1033. .1336
/note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                            /note="MIR repeat:
                                                                                                                                                                                                                                                       'note="
                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                              /clone="RP1-302D9"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                      . 933
                                                                                           . 2660
                                                                                                                                                                . 1583
                                                                                                                                                                                                                                                     MER3 repeat:
                                                                                                        repeat: matches 2593.
 repeat:
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RP1-302D9 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of clone RP1-302D9 The true left in this sequence. The true right in this sequence.
                                                                                                                                            24.
 116.
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                                                                                                                                                                                                                                                       .144 of consensus"
                                                                                                                                            .160 of consensus"
                                   .300 of consensus"
                                                                       . 309
                                                                                                                                                                               .299 of consensus"
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                                                                                                        .2661 of consensus
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Jong. For further
                                                                       consensus"
consensus"
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me 22 Contains
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/note="AluY repeat:
3653..3928
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8414. 8551
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                                 /note="MIR repeat: matches 141.
14589. .14679
                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 63. 13017. .13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: 10784. .11201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS:
complement(10249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="52 copies 2 mer ct 78 conserved" 5181. .5491
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5073. .5176
                                                                     /note="AluY repeat:
14368. .14452
                                                                                                     /note="MIR repeat:
14061. .14367
                                                                                                                                                                                                                     13699.
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13331. .13397
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12444. .12642
                                                                                                                                                                                                                                                                                                                                                                                                   12174.
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10718. .11310
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/note="MIR repeat: matches 173.
14597. .15201
                                                                                                                                              13945
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13806. .13919
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS:
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                                                                                                                                                                                                                                                                       'note="MIR repeat: matches 174.
                                                                                                                                                                                                                                                                                                                                                                                                                'note="MIR repeat: matches 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="FAM repeat: matches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 147.
                                                                                                                                                                                                                                                                                                                                                                              matches 1988.
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                                                                                                                                                             matches 77.
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                                                                                                                         matches 24.
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10706)
                                                                                      matches 1.
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                                                                                                                                                             . 189
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                                                                                                                                                                                                                                                                                                                                                                                                                  .137
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                                                                                                                                                                                                .174 of consensus"
                                                                                                                                                                                                                                                                                                                                             . 241
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                                                                                                                           .142 of consensus"
                                                                                       .301 of consensus"
                                                                                                                                                                                                                                    .302 of
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                  . 262
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                                                    .225 of consensus"
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            CysProAspIleGluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuPro
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CCTGGTGCCCCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCCCC
                                                                                                                                                                                                                                     consensus"
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                                                                                                                                                                                                                                                                                                                                                  /note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
21882. .22254
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15304. .15399
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14616. .15060
                                                                                                                                                                                                             23905. .23989
/note="MER66-internal repeat: matches
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                                                                                                                                                                                                                                                                                                                             /note="THE1B repeat: matches 1. .364 of consensus"
22302. .22537
                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSg1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                              /note="77
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="33
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="HERVFH21 repeat: matches 4657. .5784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note⇔"match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER66-internal repeat: matches
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18713. .19133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16546
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16028. .16245
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15669. .15727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Laboratory of Molecular Biology. 1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takamatsu,N., Ohba,K., Kondo,J., Kondo,N. and Shi
Hibernation-associated gene regulation of plasma
collagen-like domain in mammalian hibernators
Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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89. .679
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89. .157
                                                                                                                                                                                                                                                                               /product="HP-20"
/protein_id="BAA02351.1"
/db_xref="GI:287468"
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                                                                                                                                                                                                                                                                                                                                               /note="collagen-like domain
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(Tel:0427-78-9408,
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                                                                                                                                                                                                                                                                                                          Submitted (04-AUG-2001) Motoharu Ono, Kitasato University, Department of Biosciences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
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                                                                                                                                                                                                                                                                                             (E-mail:ms99805m@stu.sci.kitasato-u.ac.jp,
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277 (:
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               /translation="MTDAWRLAIFVLMVNVLNDQVSCSGPPGPVGYPGVPGVPGPPGPRGP
PGQPGAAGRPGDPGPKGPSVKCPCRERSAFTVKFSGRLPPPSEPVVFTEVLYNTQRDL
KASTGVFNCVEPGNYHFSFDVELYHCKVKIGLMKNHIQVMEKHQLSKNEYENASGAMI
                                                                                                                                                                         /note="synonym:Tamias
1518. .1684
                                                                                                          join(1678. .1684,2573.
/gene="HP-20"
                                                                                                                                         /gene="
                                                                                                                                                                                                                    /organism="Tamias sibiricus"
/db_xref="taxon:64680"
                                              /protein_id="BAB68362.1"
/db_xref="GI:15706342"
                                                                              /product="HP-20"
                                                                                          /codon_start=1
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                                                                                                      Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Laboratory of Molecular Biology; 1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
                                                                                                                                                                                                             Takamatsu,N., Ohba,K., Kondo,J., Kondo,N. and Shiba, Hibernation-associated gene regulation of plasma procollagen-like domain in mammalian hibernators mol. Cell. Biol. 13 (3), 1516-1521 (1993)
                                                                                                                                                                                                                                                                                                                                        Tamias sibiricus
                                                                                            Fax:0427-78-9403)
                                                                                                                                                       Direct Submission
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Takamatsu, N., Ohba, K.
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Mammalia; Eutheria;
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                            /organism="Tamias sibiricus"
/db_xref="taxon:64680"
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               /clone="pCM25-3"
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COL10A1 gene; collagen alpha 1 type
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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PGPPGIPGFPGAPGALGPPGPPGVPGIPGPQGPPGDVEKCSSRPKSAFAVKLSERPPE
PFQPIVFKEALYNQEGHFNMATGEFSCVLPGVYNFGFDIRLFQSSVKIKLMRDGIQVR
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US-09-997-610-2_COPY_18_149 (1-132) x RNO131848
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                                                              TCTGGAATCTTTACCTGTAAGATCCCAGGCATATACTATTTTTCCTATCACATCCATGTG
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HisHisCysLysValAsnIleTrpLeu-MetArgLysGlnIleLeuAlaAsnLysGluGl
                                                                                                                                                                                                                          GTAACAGGCATGCCGGTGTCCGCTTTTACTGTGATTCTTTCCAAAGCTTACCCAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGTCCTCCAGGGCGTCCTGGTCCAAGAGGTCATACTGGAGAGCCTGGTCTCCCAGGT
                                                                                     MetGlyValPheAlaCysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeu
                                                                                                                                           GGTGCTCCCATCCCATTTGATGAGATTCTGTACAACAGGCAGCAGCACTATGACCCAAGA 600
                                                                                                                                                                   PheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                           CCTCCAGGACCCCCAGGACCTCCAGGACCTCCCAGCCAAGCAGTCATACCTGATGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marks,S.C. Jr., Lundmark,C., Christersson,C., Wurtz,T., Odgren,P.R., Seifert,M.F., Mackay,C.A., Mason-Savas,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-DEC-1998) Wurtz T., Karolinska Institutet, Box 4064,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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LYSSEYVHSSFSGFLVAPI"
1 462 c 427 g 498 t
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/protein_id="CAA10518.1"
/db_xref="GI:4090263"
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/db_xref="taxon:10116"
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Best Local Similarity:
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   LeuProGln----
                                  AGCGGAGAACCTGGCTTGCCAGGTCCCCCGGTCCTCCTGGTCCCCCTGGCCAATCCACA 1698
                                                                  AlaGlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGly
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J. Bi
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Chicken red blood cell DNA, clone pYN92E1;
cDNA to mRNA, clone pYN3116.
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] has as yet not determined the start codon of gene. The open reading frame starts at position several 'atg' codons (starting at positions 190, 310) following the 'taa' at position 163.
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                                                                                                                                                                                                                                                                              /note="a in DNA; t in a 635 c 659 g upstream of BamHI site
                                                                                                                                                                                                                                                                                                                                                                                                                       KPGLPGMKGHRGPEGPPGFPGPKGDQGPAGVPGELGPAGPQGNMGPQGLKGLPGENGLPGPKGDMGPVGPAGFPGAKGERGLPGLDGKPGYPGELGPKGDPKGHPGLPGQKGDTGHAGPFGLPGPVGPQGVKGVPGINGEPGPRGPSGIPGVRGPIGPPGMPGAPGAKGEAGAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="RPGFGSPGPDGPPGPLGPPGFSTVGKLGMPGLPGKPGERGLNGE
KGEAGPVGLEGARGPGGPPG1FGPAGLSVLGKPGPGGPPGACGERGPPGSKGEFGVPG
INGOKGEMGFGVPGRFRGLFGPGGPOGLPGSAGIGKPGENGLPGCPGKGDRGLPG
INGOKGEMGFGVPGRPGEPGEVGIGKPGPMGPPGPAGIPGAKGLPGPAGLPGSPGLPGFG
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FTCRIPGLYYFSYHVHAKGTNVWVALYKNGSPVMYTYDEYQKGYLDQPQAVLSLISWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="type X collagen"
/protein_id="AAA48736.1"
/db_xref="GI:211700"
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635 c 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=3
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/db_xref="taxon:9031"
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                                                                                                                                          2.59e-06
167.50
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TyrThrGlyGluIleSerGlu--
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166. There are
214, 256, 274 and
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Callosciurus caniceps DNA, clone:lambda
Callosciurus caniceps
                                                                                                                                                                                                                                                                                            Submitted (06-AUG-2001) Nobuhiko Takamatsu, Kitasato University, Department of Biosciences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:takamatu@jet.sci.kitasato-u.ac.jp, Tel:81427789408,
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    Kojima,M., Shiba,T., Kondo,N. and Takamatsu,N. The tree squirrel HP-25 gene is a pseudogene Eur. J. Biochem. 268 (22), 5997-6002 (2001)
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                /pseudo
128
                                                                         /product="HP-25" 39. .>559
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join(AB067813.1:1503. .)
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Alignment Scores:

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                                                                                                                                                                                                                                          Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Laboratory of Molecular Biology; 1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
                                                                                                                                                                                                                                                                                                                                                        Takamatsu,N., Ohba,K., Kondo,J., Kondo,N. and Shiba,T. Hibernation-associated gene regulation of plasma prote collagen-like domain in mammallan hibernators coll. Cell. Biol. 13 (3), 1516-1521 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
Tamias asiaticus liver cDNA to mRNA, clone:pCM27-3.
Tamias sibiricus
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65. .712
                                                                                                                                                /db_xref="taxon:64680"
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                                                                                                                                                                                /organism="Tamias sibiricus"
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                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            Cancer gene determination
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                                                                                                                                       Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Horrigan,S., Soppet,D.R. and Weaver,Z.
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              /organism="Homo sapiens"
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91231001
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                                                                                                                                                                                                                                           Biology, Harv
                                                                                                                                                                                                                                                    Submitted (05-FEB-1991) B.R. Olsen, Dept of Anatomy and, Cellular Biology, Harvard Medical School, 220 Longwood Avenue, Boston MA
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                                                  /map="3q12-3q13.1"
/clone="YMh801"
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1. .2235
 /gene="COL8A1"
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                                     /clone_lib="genomic
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J05042.1 GI:164895 alpha-1 type VIII collagen; basement membrane protein
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IlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPhe 79
                                      GAGATGCCTGCCTTTACCGCCGAGCTGACGGCACCCTTCCCCCGGTGGGGGGCCCCGATA 2079
                                                                         GluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLysProIle 59
                                                                                                                    GGGGTAAAAACTCCTCACGCCTATGCGGCCAAGAAAGGCAAGAACGGCGGGCCCAGCCTAT 2019
                                                                                                                                                           ---ThrLysCysPro------
                                                                                                                                                                                                                                                                            GGCCAGCCTGGCCTCCCAGGCCCCCAGGCCCTCCAGGGCCCCCAGCTGTG 1899
                                                                                                                                                                                                                                                                                                                 GlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGlyLeu
                                                                                                                                                                                                                                       Yamaguchi,N., Benya,P.D., van der Rest,M. and Ninomiya,Y.
The cloning and sequencing of alpha 1(VIII) collagen cDNAs
demonstrate that type VIII collagen is a short chain collagen and
contains triple-helical and carboxyl-terminal non-triple-helical
domains similar to those of type X collagen
J. Biol. Chem. 264 (27), 16022-16029 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Draft entry and computer-readable copy of sequence submitted by Y.Ninomiya 23\text{-AUG-}89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit (strain New Zealand white) young adult cornea endothelial cells, cDNA to mRNA, clone pCE1230 and NK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89380199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"alpha-1 (VIII) collagen signal peptide" 241. .2412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAAKKGKNGGPAYEMPAFTAELTA
PFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVMVALFKNN
EPVMYTYDEYKKGFLDQASGSAVLLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPKKGKEIPLÄSLRGEQGPRGEPGPRGPPGPPGLPGQGIPGIKGKPGPQGYPGVGKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA31204.1"
/db_xref="GI:164896"
/translation="MAVPPGPPQLLQYLLTISLGSIRLIQAGAYYGIKPLPPQIPPQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="alpha-1 (VIII) collagen"
719 c 768 g 392 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha-1 (VIII) collagen precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
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32.61%
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
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Submitted (04-SEP-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Series: IRAK Plate: 14 Row: a Column: 8
This clone was selected for full length sequencing passed the following selection criteria: matched mp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2506)
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                                    GLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPGPKGEPGLQGFPGKPGFLGEVGPPGMRGLPGPPGIGGPSGPMRGLPGPDGLQGPPGIPGIGGPSGPMRGLPGPPGLQGPGLQGPPGIPGIGGPSGPMRGLPGPDQCLQGPPGIPGIGGPSGPMRGLPGPMGPPGLPGPMGPPGAIGFPGPPG
                                                                                                                      GMPOMPGKPOAMGMPOAKGEIGOKGEIGPMGIPGPPGPPGPHGLIPGICKPGGPGLIPGO
PGPKGDRGPKGLIPGPQCLIRGPKGDKGFGMPGAAPGVKGPPGMPGDPGIPGOPGFPGKFG
TGFPFGPQGPLGKFGAPGEEPGPQGPIGVPGVQGPPGIPGIFGCPGIPGOPGFPGGKG
EQGLIPGLIPGPPGLIPGIGKPGFPGFFGKDRGMGGVPGALGPRGEKGPIGAPGIGGPPGEP
                                                                                                                                                                                                                                                                                          /product="unknown (protein for MGC:9568)"
/protein_id="AAH13581.1"
/db_xref="GI:488904"
/translation="MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGIKPLPPQIPPQM
/translation="MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGIKPLPPQIPPQM
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PPQIPOYQPLGQQVPHMPLAKDGLAMGKEPGPGPGLPGHGIPGIKGKPGPQGYPGVGKP
AVPKKGKEIPLASLRGEOGPRGEPGBRGPGBPGLPGHGIPGIKGKPGPQGYPGVGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector:
238. .2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Lung, lar
/clone_lib="NIH_MGC_68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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IGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGLPGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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clone MGC:9568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             large cell carcinoma"
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IMAGE:3875911, mRNA, complete
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                  Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavzos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cheveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Hart, M., Harlak, P., Hawes, A., He, X., Garner, M., Gunaratne, P., Hawes, A., He, X., Hernander, T., Harris, K., Hart, M., Harlak, P., Hawes, A., He, X., Garner, M., Gunaratne, P., Hawes, A., He, X., Garner, M., G
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      Hodgson, A.,
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Hogues, M.,
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Ma.J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, S., Mitchell, T., Mohabbat, K.,
Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D.,
Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D.,
Nelson, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Scherer, S.,
Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E.,
Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatte, A.,
Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, G.,
Taylor, T., Telfrod, B., Thomas, N., Tang, H., Tansey, J., Taylor, C.,
Warren, R., Washington, C., Wattlington, S., Walliams, G.,
Warren, R., Washington, C., Wattlington, S., Walliams, G.,
Wul, Y., Shou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
Gibbs P.
Submitted (29-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 1, 2002 this sequence version replaced gi:18958589. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-MAR-2002) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 117000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAY-2000) of Molecular and Human G
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Direct Submission
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Baylor Plaza, Houston,
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Direct Submission
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Genetics, Baylor College
TX 77030, USA
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of Medicine, One
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REFERENCE AUTHORS

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

COMMENT

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AUTHORS

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# ANNOTATION OF FEATURES

STSs are identified using ePCR (Genome Res. 7: of a local database that includes entries from db local mapping efforts.
Repeats are identified using RepeatMasker (A. Res. 7:541-550) from dbSTS, GDB, searches

Smit and P. Green

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are identical matches are annotated as similar. Sequences that are not

FEATURES

source

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUALSTAT-REPORT
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complement(16209.
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                         /rpt_family="Charlielb"
complement(9345. .9645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3024. .3183)
/rpt_family="L2"
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/rpt_family="L2"
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11973
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/db_xref="taxon:9606"
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_9700
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DB:
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                                                                                                                           GGGGCAACGTGTGGGTT-----
          Z82198
Z82198.2 GI:6572207
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27309.
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20770 .20907
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162.50
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30.43%
22.82%
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US-09-997-610-2_COPY_18_149 (1-132) x AC069222 (1-117000)
                                                                                                                                                                                                                                                         71969 ACCTGTGAGGTCCCTGGTGTCTACTTTGCATACCACGTT------CACTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GluArgSerAlaPheThrValLysLeuSerGlyLysLeuProLeuProPheLysProIle 59
                                                                                                                                                                                                                                                                                                                                                                                                      60 IlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLysGluAlaMetGlyValPhe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 -----ProGlnTyrThrGlyGluIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GlyProProAlaHisProArgProProGluGluValGlyProProGlyAlaProGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGATGCCTGCATTTACCGCCGAGCTAACCGCACCTTTCCCACCGGTGGGGGCCCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTGAAACCCCCCCATGCCTACGGGGCTAAGAAAGGCAAGAATGGAGGGCCAGCCTAT 72090
                                                                                                                                                                                                                                                                                                       AlaCysArgValProGlyAsnTyrTyrSerSerPheAspValGluLeuH1sHisCysLys 99
                                                                                                                                                                                                                                                                                                                                                           AAGTTTAACAAACTGCTGTATAACGGCAGACAGAACTACAACCCGCAGACAGGCATCTTC
                                                                                                                                                                                                        ---ValAsnIleTrpLeuMetArgLysGlnIleLeuAlaAsnLysGluGluIle 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SerGluMetThrLysCysProCysProAspIle
145880 bp DNA linear PRI 12-DEC-19: Human DNA sequence from clone RP1-302D9 on chromosome 22 Contains GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MER5A"
23517. .23607
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/rpt_family="MER1B"
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complement/>>^~
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20164. .20228
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19297. .19426
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4. .270<^
                                                                                                                                                            --GCTCTATTCAAGAACAACGAGCCCGTG 71874
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Indels:
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Dec 13, 1999 this sequence version replaced gi:3164067. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone RP1-302D9 The true left end of clone CTA-282F2 is at 69682 in this sequence. The true right end of clone CTA-415G2 is at 55167 in this sequence.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chr22
RPI-302D9 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22 constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bridgeman,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188.
                                                                                                                   /note="MLT1E repeat: matches 116.
3344. .3652
                                                                                                                                                           /note="AluSq repeat: matches 2.
3323. .3343
                                                                                                                                                                                                     2684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/chromosome="22"
/note="THE1B repeat: matches 3.
4279. .4485
                                                        /note="MLT1E repeat: matches 136.
                                                                                                  /note="Aluy
                                                                                                                                                                                                                        /note="AluSc repeat: matches 3.
                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2593.
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                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER3 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER3 repeat: matches 144. .209
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/clone_lib="RPCI-1"
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13017. .13369
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12444. .12642
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7775. .8060
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                                                            14868.
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12174. .12445
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10718. .11310
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14368. .14452
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7482. .7754
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                                                                                                  14616.
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14061. .14367
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                                     'note≔"MIR repeat: matches 49.
                                                                                                                     note="match: GSS:
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13806. .13919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: STS: Em:G49301"
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                                                                                                                                                             matches 173.
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2112.
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                                                                                                                                                                                       GlyLeuProGlnTyrThrGlyGluIleSerGluMetThrLysCysProCysProAspIle
                                           GTGCCCTTCTAGCCCATTGTCTTCAAGGAAGCCCTTTATAATACTCAGTTCCATTTCCAT 90780
                                                                                                                                                               GGAATCCCTGGTTTCTATGGAGAA-----CAAAGACCAAGAGCAGTAGAAGGAGATATT
                                                                        LeuProPheLysProIleIlePheThrGlyValLeuTyrAsnAlaGlnArgAspLeuLys
                                                                                                      GAAAAACGTTCATCCCCACCAAGATCTGCATTTGTGGTGAAACTGATCGGACCCCTCCCA 90840
                                                                                                                                      Glu-----
                                                                                                                                                                                                                                                                                                                                                                                                     consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER66-internal repeat: matches 4919. .4993 of
consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLT1B repeat: matches 15490. .15662
                                                                                                                                                                                                                                                                                                                                                                         /note="MER66-internal repeat: matches 3017.
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER66-internal
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluSp repeat:
22851. .23801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MER66-internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="THE1B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="HUERS-P3 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSg1 repeat: matches 1. .306 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20682. .21008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="33 copies 2 mer ta 68 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="HERVFH21 repeat: matches 4657. .5784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: 19251. .19719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER66-internal repeat: matches 4548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MSTA repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"MLT1B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="AluSc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1B repeat:
15728. .16027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSg1 repeat: matches 2.
15669. .15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluJb repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="match: GSS: Em:B14179"
                                                                                                                                                                                                                                                        0.000595
162.50
50.89%
37.50%
22.82%
                                                                                                                     ----ArgSerAlaPheThrValLysLeuSerGlyLysLeuPro
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Conservative:
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                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches
                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .29 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  .313
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                                                                                                                                                                                                                                                        42
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucler,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Mansey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Perey,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuHisHisCysLysValAsnIleTrpLeuMetArgLysGlnIle---LeuAlaAsn
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Baylor Plaza, Houston,
3 (bases 1 to 152354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
      Worley, K.C.
Direct Submission
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On Jul 18, 2002 this sequence version replaced gi:20564266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draff_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 142151 bases at least Q40
Consensus quality: 147764 bases at least Q30
Consensus quality: 152093 bases at least Q20
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Search completed: February 19, Job time: 1969.21 secs

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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UI-R-CAO-baw-b-08-0-UI.S1 UI-R-CAO Rattus norvegicus cDNA clone UI-R-CAO-baw-b-08-0-UI 3', mRNA sequence.
BE121287
BE121287.1 GI:8513392
                                                                                     Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A
                                                                                                                                                                                                                     97044477
                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches
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Bonaldo, M.F., Lenno
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BI323061
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                                                                                                                                                                                                                                                                                      1 (bases 1 to 461)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI323061 461 bp mRNA linear EST 30-JUL-
kt68h01.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR:Q19079 Q19079 COSMID
EGAP7. [1] ;contains element MSR1 repetitive element ;, mRNA
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongyloides ratti. Strongyloides ratti
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                                                                                                                                                                                                                 The Washington Univ. Nematode EST Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloididae; Strongyloides.
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//clone_lib="UI-R-CAO"
//lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG310518 675 bp mRNA linear EST 23-FEB-20 SWOV3MCAM56C07SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCAM56C07 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu) at WcSarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
                                                                                                                                                                                                                                                                                                                          Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                 College, Northampton,
                                                                                                                                                                                                                                                                                                                                                                                                                           Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Steven A. Williams Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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//lab_host="DHIOB"
//lab_host="DH
/clone="SWOv3MCAM56C07"
/clone_lib="Onchocerca"
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/db_xref="taxon:34506"
                                                           /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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                                                                                                                                              /organism="Onchocerca volvulus"
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                             Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clu
196F02 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                        Direct Submission
                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome
                                                                                                                                                                                                                                                                                             Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          slustigm@nybc.org)."
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco
Xho I; Filarial nematode parasite of humans. T
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/dev_stage="molting L3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zehn1908.seq.F Zebrafish CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                     PCR PRIMER'S
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
FORWARD: 5' CCAGTGAATTCTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brigham and Women's Hospital
Harvard Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an Embryonic Zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                             Email: cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                              75 Francis St. Boston, MA 02115, Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification and Characterization of Expressed Sequence Tags from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio
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                                                                                        /clone_lib="Zebrafish Embryonic Heart cDNA Library"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XLI-Blue mrp"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
ECORI; Site_2: Xhoi; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."
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a 211 c
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/clone="196F02"
                                                                                      Express vector
                                                                                                                                                                                                                                                              /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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41.0%;
71.0%;
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Pred. No. 8
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Pred. No. 9;
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                                                             kq42d08.yl TBN95TM-SSR Strongyloides stercoralls cDNA 5' similar to contains element MSRl repetitive element ; mRNA sequence.
BE581111
BE581111.1 GI:9832053
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Caenorhadditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Deloderinae; Caenorhadditis
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             Strongyloides stercoralis.
Strongyloides stercoralis
Eukaryota; Metazoa; Nemato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1994)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toward an expression map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Biology Lab.
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                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole animal"
/dev_stage="varied"
116 c 105 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk73c7"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
                                                                                                                                                                                                                                                                                                             41.0%;
64.1%;
  Strongyloididae;
Nematoda; Chromadorea; Rhabditida; crongyloididae; Strongyloides.
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BJ136441.1
                                                                                                        Caenorhabditis elegans.
            Unpublished (2002
                                         and Sugano,S.
                                                     Kohara, Y., Shin-i, T.,
                                                                                                                                      EST
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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64.1%;
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267 GGACCACCAGGACCTCCAGGGCCACCAGGATTTCCAGGAGAACCAGGAACACCAGGATTA 326
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea;
; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The library was constructed by Dr. Thomas Nut
NIAID, NIH (tnutman@nih.gov). DNA Sequencing
University Genome Sequencing Center St. Louis
High quality sequence stop: 416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Washington Univ. Nematode
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//note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
//note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
//note="Vector: Real XR (Stratagene); Site_1:
//note="Vector: Real XR (Stratagene); Site_1:
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//note="
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/strain="Rhabditiform larvae obtained
/db_xref="taxon:6248"
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                                                                                              Thierry-Mieg,J.,
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C.elegans
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                                                                                              Thierry-Mieg, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
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BJ108893
BJ108893.1 GI:18268921
EST
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                                                                                                                                                                                                                                                                                                                                               A complementary view of the C.elegans genome Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                   Tel:
                                                                                                                                                                                                                                                                   Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                     Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditidae; Peloderinae; (bases 1 to 726)
                                                                                                                                                                                                                                                                                                                                                                                       Sugano, S.
                                                                                                                                                                                                                                   81-559-81-6855
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                                                                                                                                                                                                             tshini@genes.nig.ac.jp
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RNA isolated from both hermaphrodite and male N2 worms
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
5 others
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elegans L1 stage"
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/dev_stage="L1"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
                                                                                                                                     /strain="N2"
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                                                                       /clone_lib="unpublished oligo-capped
                                                                                                                 /db_xref="taxon:6239"
                                                                                                                                                       /organism="Caenorhabditis
                                                                                                                                                                                             Location/Qualifiers
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64.1%;
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13b05 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes expressed in young adult 
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome@smith.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWYD25CAU05E10SK Brugia malayi young adult
(SAW99MLW-BMYD25) Brugia malayi cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 64.7
50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 613)
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                                                                                                    181
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                                                                                                                                                      /dev_stage="young adult, twenty five days after infection"
/lab_host="xil-Blue MRF'"
/note="vector: Lambda Uni-ZAR XR; Site_1: Eco RI; Site_2:
/note="vector: Lambda Uni-ZAR XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.

MRNA was prepared from young adult worms isolated from
the peritoneal cavity of jirds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 6.2 x 105 independent recombinants
and the average insert size is approx.1101bp. The library
was constructed by Michelle Lizotte-Wanlewski. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

a 219 c 192 g 125 t 1 others
                                                                                                    genome@neal.smith.edu.
139 c 175 g
                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmYD25)"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Brugia malayi"
/db_xref="taxon:6279"
                                                                                                                                       library is available from Dr. S.A. Williams,
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="SWYD25CAU05E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                    40.78;
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64.1%;
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Score 33; DB Pred. No. 11; 0; Mismatches
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Pred. No. 9
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                                       Length 613;
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day 25 cDNA
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Similarity

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BASE COUNT
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BM896730
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  Query Match
Best Local
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
    Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
    Dante,M., Marra,M., Hillier,L., Franklin,C., Tsagareishvili,R.,
    Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.,
    Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
    Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM896730 417 bp mRNA linear EST 12-MAR-20ph47c02.yl Ostertagia ostertagi L4 pAMPl vl Ostertagia ostertagi cDNA 5' similar to TR:019079 019079 COSMID EGAP7. [1] ;contains element MSR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University Genome Sequencing Center Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at Washington University, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Washington Univ. Nematode EST Project, 1999 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ostertagia ostertagi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library was constructed by Claire Murphy and Dr. James McCarter
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 395.
                                                                                                  85
                                                                                                                                                                                                                                                                                                     /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Claire Murphy and Dr. James McCartter at Washington University, St. Louis. The CDNA wass made by using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarree of the USDA, Beltsville, MD
                                                                                                                                                               (lgasbarr@anri.barc.usda.gov). Late fourth stage larvae were recovered 10 days after infection of young calves with Ostertagia L3. The calves were killed and the abomasa (gastric glands) were recovered and washed extensively and then placed in a Baermann apparatus containing warm PBS for approximately 4 hours. The L4 that migrated from the
                                                                                                in liquid nitrogen."
139 c 137 g
                                                                                                                                             tissues were washed extensively,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Ostertagia ostertagi L4 pAMP1 v1"
/dev_stage="L4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
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  40
64
55.5
Score
Pred.
32.8;
No. 12;
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                      DB
                      14;
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                    Length 417
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                      534
                                                                 1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCCTCCTGGTGCACCAGGTTTA 60
                      GGACCGCCTGGACCTCCCGGTCCACCTGGACAAGCGGGACCACCTGGAGAACCAGGAGCA 593
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Query Match
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46; Conser
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ548321 698 bp mRNA linear EST 17-JUN-200: rd24c08.y1 meloidogyne incognita egg SL1 TOPO v1 meloidogyne incognita cDNA 5' similar to TR:018302 0,018302 C29F4.1 PROTEIN. [1] contains element MSR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at Washington University, St. Louis. Meloidogyne incognita were provided by Andrew Kloek of Divergence Inc., St. Louis Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The library was constructed by Claire Murphy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Washington Univ. Nematode EST Project, Unpublished (1999)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        southern root-knot nematode.
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                                                                                                                   Site_2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Meloidogyne incognita eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO." a 190 c 191 g 142 t 1 others
                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (Invitrogen)"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Meloidogyne incognita egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Meloidogyne incognita"
/db_xref="taxon:6306"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="egg"
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CCACAATA 68

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TITLE
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI3891 row: h column: 17
                                                                                                                                                 BQ258938
BQ258938.1 GI:20459702
EST.
                                                                                                                                                                                                                                      BQ258938 494 bp mRNA linear EST 06-MAY. faa25e07.yl zebrafish fin day3 regeneration Danio rerio cDNA cl. 5910229 5' similar to TR:093486 093486 ALPHA 3 TYPE I COLLAGEN CONTAINS PTR5.b2 MSR1 repetitive element; mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:10090"
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             Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes
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                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGACCCCCAGG 170
                                                                                                                                                                                                               499 bp mRNA linear EST 20-MAR-20(LM24HW0134 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone LM-24-HW-011-34 (5'), mRNA sequence.
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                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                        Bos taurus
                                                                                                                                                                                              BM967732.1
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
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                                             Bovidae; Bovinae; Bos.
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                      (bases 1 to 499)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"vector: pBK-CMV; Site_1: ECORI; Site_2: XhOI; 1st strand cDNA primed with (GA)10ACTAGTCTGAC[7]1B, followed by second strand synthesis, and ligated to 5 adapter (5')-aattcggcacgag-3', 3'-gccgtgctc-5'. cDNA was cloned directionally (ECORI/XhOI) into Stratagene Zap express lambda phage arms. Mass invivo excision done to obtain inserts in pBK-CMV phagemid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="zebrafish fin day3 regeneration"
/sex="mixed male and female"
/tissue_type="3 day fin regenerates"
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/clone="5910229"
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Lee, H.K., Chung, E.R.,
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COMMENT
Search completed: February 20, Job time: 210.778 secs
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Gene Expression Profiling of the Bovine skeletal muscle
Unpublished (2002)
Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Omockchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1593
Fax: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhyoon@rda.go.kr
Insert Length: 499 Std Error: 0.00
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POLYA=No.
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/note="Norgan: skeletal muscle; Vector: Uni-ZAPXR; Site_1:
ECORI; Site_2: Xho I"
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  seq
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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	atch bal s	FILING DATE: Decembe CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: FILING DATE: ATTORNEY/AGENT INFORMAT NAME: John F. Freema REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET. REFERENCE/DOCKET.	ADDRESSEE: Fish & Riche STREET: 225 Franklin St CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02210-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 Diske COMPUTER: IBM PS/2 Mode COMPUTER: WOrdPerfect COMPUTER: WordPerfect COMPUTER: WordPerfect COMPUTER: MODELICATION DATA: ADDITATION STREEM: MS-COUNTRY COURTERNT APPLICATION DATA:	LT 1 8-159-784-4 8-159-784-4 quence 4, Applicatic quence 1, Applicatic ENERAL INFORMATION: ENERGY BOOK APPLICANT: Bjorn APPLICANT: Bjorn ITTLE OF INVENTION: NUMBER OF SEQUENCES COMPRESSION	%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%	
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CCCCAGGO     CAAGGGCO	37.5%; 71.4%; ative	December 1, 199 ON DATA: UNBER: INFORMATION: Freeman VUMBER: ON INFORMATION: ON INFORMATION 617) 542-5070 7) 542-8906 4 EQ ID NO: 4: TERISTICS: TERISTICS: c acid single near	& Richardson & Richardson klin Street etts  ORM:     Diskette, 1     Diskette, 2     MS-DOS (Ver rfect (Versic DATA:     DATA:     DOS (1967)	n US/0815978 Olsen NOVEL COLL	2504 32504 32504 32504 42505 12505 12505 12505 12505 12505 12505 12505 12505 12505 12505 12506 125	
GGACCTCCAGCACACCCCAGGCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGG 	0	24 93	4.4 or	L5978	US-08-6 US-08-7 US-08-7 US-09-3 US-08-5 US-08-4 PCT-US9 PCT	
GAAGTGGG          GAAGTGGG	Score 30.4; DB Pred. No. 0.42; Mismatches	/170001	4 Mb 55SX on 5.0) 5.1)	ALIGNMENTS 4 AGEN AND USES	US-08-682-853A-3 US-08-759-038-3 US-08-758-314-3 US-08-758-314-3 US-09-350-309-3 US-08-520-946-3 US-08-458-819-9 US-08-458-819-9 US-08-459-383-30 US-08-459-383-30 US-08-459-383-31 US-09-428-711A-15 US-09-428-711A-15 US-09-386-536-2 US-08-627-151A-15 US-09-366-536-2 US-08-627-151A-15 US-09-366-510-1	
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; Sequence 20, Application US/09029348

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US-09-342-681C-14
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-681C-7
                   RESULT 4
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APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09342681C Patent No. 6355782 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/092,279
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/112,366
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/342,681C CURRENT FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zonana et al. TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins FILE REFERENCE: 52978
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                                                                        CCTGGAATTCCAGGAACAA 397
                                                                                                                                                                                                                   36.3%;
1 Similarity 60.8%;
48; Conservation
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Similarity 60.5%;
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US-09-342-681C-1
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LENGTH: 1176
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Patent No. 6355782
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TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia

FILE REFERENCE: 52978

CURRENT APPLICATION NUMBER: US/09/342,681C

CURRENT ETLING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/092,279

PRIOR FILING DATE: 1998-07-09

PRIOR APPLICATION NUMBER: 60/112,366

PRIOR FILING DATE: 1998-12-15
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TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978
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PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
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                                                                                                                                                                                                                                                                                 LENGTH: 1574
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (242)..(1417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 CCTGGAATTCCAGGAACAA 634
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                                                                    797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCACAATATACAGGAGAAA 79
                               61 CCACAATATACAGGAGAAA 79
                                                                                                                                                          Local Similarity
                                                                                                    1 GGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCCTCCTGGTGCACCAGGTTTA 60
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Local Similarity 60.8%;
                                                                    GGCCCTCCAGGACCCCCAGGACCTCCAGGACCCCCAGGGACTCCCAGGGATT 856
CCTGGAATTCCAGGAACAA 875
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                                                                                                                                           Conservative
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                                                                                                                                                          36.3%;
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                                                                                                                                                                            DB 4;
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US-09-134-001C-635/c

; Sequence 635, Application US/09134001C
; Sequence 636, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynon Doucette-Stamm et al
; APPLICANT: Lynon Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-647
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RESULT 8
US-09-134-001C-726
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LENGTH: 513
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LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION UNMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEO ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                      238
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                                                                                                                             61 CCACAATATACAGGAGAA 78
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                                                                                      CCAGCAGAACCAGGTAAA 221
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Pred. No. 3.
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Pred. No. 3.7;
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                                                             RESULT 10
US-09-134-001C-693
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RESULT 9
US-09-134-001C-624/c
US-09-134-001C-624/c
; Sequence 624, Application US/09134001C
- barent No. 6380370
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                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 726
LENGTH: 585
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                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT ENFLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                LENGTH: 810
TYPE: DNA
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                                                                                    266 GGTACGCCAGCAGAACCAGGTACGCCAGCAGCAGCTAAACCAGCGGAACCAGGTACG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 CCAGCAGAACCAGGTAAA 347
206 CCAGCAGAACCAGGTAAA 189
                                       61 CCACAATATACAGGAGAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCACAATATACAGGAGAA 78
                                                                                                                                                                                        Match 33.1%;
Local Similarity 59.0%;
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Local Similarity 59.0%;
les 46; Conservative
                                                                                                                         1 GGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60
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                                                                                                                                                                    Conservative
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Pred. No. 4.4;
                                                                                                                                                                    Mismatches
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Patent No. 6380370 GENERAL INFORMATION:

Sequence 693,

93, Application US/09134001C 6380370

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RESULT 12
5510466-1
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5510466-3
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-693
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                                                                   ;Patent No. 5510466
; APPLICANT: KREIGER,
; TITLE OF INVENTION:
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                                                      THERETO
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Best Local Similarity 55...
46; Conservative
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SEQ ID NO 693
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                NUMBER OF SEQUENCES: 12 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KREIGER, TITLE OF INVENTION:
                                                                                                                                                                                               877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                         817 GGTCCTCCTGGACCTCCAGGTGAAAAAGGAGATAGAGGCCCTCCTGGACAAAATGGTATA 876
                                                                                                                                                                                                                     61 CCACAATATACAGGAGAAATA 81
                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
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 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 997,113 FILING DATE: 24-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGTTTA 60
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                                                                                                                                                                                             CCAGGCTTTCCAGGTCTAATA 897
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                                                                   MONTY; KODAMA, TATSUHIKO SCAVENGER RECEPTOR PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONTY; KODAMA, TATSUHIKO SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
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59.0%;
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US/08/307,40C
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                                                                                                                                                                                                                                                                                                                                                Score 26.6; D
Pred. No. 6.1;
                                                                   RECEPTOR PROTEIN AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                 DB 6;
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                                                                                                                                                                                                                                                                                                                                                                   Length 1588;
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US-08-648-657-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 633 West Fifth Street
STREET: 630 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION STRUCTURE APPLICATION S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 900/1 200
COMPUTER READABLE FORM:
VENTIM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: US 08/455,686 FILING DATE: May 31, 1995 ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Davis, Maria
APPLICANT: Moffett, R. Bruce
APPLICANT: Fuller, Carl W.
TITLE OF INVENTION: THERMOST/
TITLE OF INVENTION: POLYMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                             TELEFAX: (*-
TELEFAX: 67-3510
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                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                              STRANDEDNESS:
                                                                                            LENGTH:
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47; Conservative
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                                                          nucleic acid
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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; LOCATION:
PCT-US95-14418-3
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US-08-648-657-14
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                                                                                                                                                                                                                                     IELEX: 25.3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1794 bass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.5
Conservative
                                                                                               Matches
                                                                                                                        Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT. INFORMATION:
NAME: GASS, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                1595
 1655
                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                     FEATURE:
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                       69 TAC 71
                                                                                                                                                                                                                                                                                     TELEPHONE: 314, TELEPHONE: 312/474-0448
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                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                            Local Similarity
                                                                                                                                                                                                              TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATA 68
TCC 1657
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                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application PC/TUS9514418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                               Conservative
                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FY4
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Pred. No. 8.4;
0; Mismatches
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                                                                                                           Score 26.2;
Pred. No. 8
                                                                                               ed. No. 8.5;
Mismatches
                                                                                                                        DB
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                                                                                                                     Length 1794;
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Search completed: February 19, 2003, 22:58:45
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PCT-US95-15327-3
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                                                                                                                                                                            Matches
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                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                        1655 TCC 1657
                                                                                                                   1595 AGCTCTTCCCCCCGCCTCCGGGAGATGGGGGCCCGCATGCTCCTCCAGGTCCACGACGAGC 1654
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 1794 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Chicago
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                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                      69 TAC 71
                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gass, David A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                               9 AGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATA 68
                                                                                                                                                                            40;
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Illinois
                                                                                                                                                                                                                                                                                                                                                     1794 base pairs
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Thermus Flavus DNA Polymerase
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Tower, 233
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South Wacker
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                                                                                                                                           AAL44066
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6506.903 Million cell updates/sec
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            Human polynucleoti
Human immune/haema
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                                                                                                       Human
                                                                                                                       Mouse
                                                                                                                                           Human
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alpha-1 coll
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                                                                    Tumour Endot
polynucleoti
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Human full-length	AAS44690	22	9483	σ.		OI
Human Tumour Endot	10	24	9192	36.3	29.4	4.
Human colon cancer	AAH33347	22	4062	σ.	9.	ω
EDA1-II	ABL51009	24	1574	6.	9.	N
Ι	ABL51020	24	1176	6.	9	_
	ABL51013	24	821	٥.	9	0
Human polynucleoti	AAI58233	22	6674	σ.	9.	9
encoding	AAS34830	22	1619	6.		80
9	AAS27365	22	1619	٥,	9.	7
Human benign prost	ABK64501	24	9287	6	9.	σ
nove	AAS79378	23	5466	6.	9.	G
N	ABL92101	24	5460	٥.	9.	4
en type	ABA83117	22	5460	σ.	9	ω
70	AAT16508	17	5460	6.	9	N
O .	AAD06578	22	4428	6.	9	_
	AAD06575	22	4428	6.	9.	0
alpha1(II	AAD06574	22	4428	6.	9	9
g	AAT59892	18	1881	6.	9.	æ
ğ	AAF44902	22	994	6.	9.	7
#28	ABK44088	24	823	٥.	9	σ
#5	ABK44065	24	780	6.	9.	5
#52	ABK44112	24	659	٥.	9	4
#71	ABK44131	24	658	6	9.	ω
#69	ABK44129	24	656	6.	9.	N
#68	ABK44128	24	655	6.	9.	_
<b>#</b> 53	ABK44113	24	653	6	9	0
#66	ABK44126	24	648	٥.	9	ø
<b>#</b> 51	ABK44111	24	617	6.	9	æ
#47 en	ABK44107	24	561	ა	9	7
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cDNA encoding nove	Z	22	2686	7.	30	u
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#2178 used t	56	24	3394	7		_
Human alphal (XVII	AAX78379	20	ω 9	7.	30.4	0

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## ALIGNMENTS

RESULT 1

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AAL44066
ID AAL4
Human; gene; ss; gene therapy; genset metabolic gene; GMG-7A; GMG-7B; GMG-8; GMG-9; GMG-10; CMG-11; metabolic-related disorder; obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; heart disease; cardiac insufficiency; coronary insufficiency; high blood pressure; insulin sensitiser;
                      18-JUL-2002.
                                               WO200255694-A2.
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                        Human genset metabolic gene (GMG-9) cDNA sequence
                                                                                                                                                                                                                                                                                                                  27-SEP-2002
                                                                                                                                                                                                                                                                                                                                          AAL44066;
                                                                                                                                                                                    non·insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                   AAL44066 standard; cDNA; 1338
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                                                                                              /partial
                                                                                                                                   Location/Qualifiers
                                                                     /product= "Human GMG-9 protein"
/note= "No stop codon is given"
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15-JAN-2002; 2002WO-IB01215.

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         Examining the ischemic condition (e.g. expression levels of particular genes by determining the expression profile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or preventing a metabolic-related disease or disorder, e. obesity, impaired glucose tolerance, insulin resistance, Syndrome Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
genes
                                                                         WPI;
                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                         (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                       18-MAY-2001; 2001WO-JP04192
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                                                                                                                                                                                                                                                                           vasospastic
                                                                                                                                                                                                                                                                                        Mouse;
                                                                                                                                                                                                                                                                                                              Mouse ischaemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1338 BP; 359 A; 288
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   determining the 
les -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention comprises the amino acid and coding sequences of six human set metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11)
                                                            2002-034733/04
DB; ABB57334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAATGTCCTGGTGCCCCAGGTTTACCACAATATACAGGAGAAATA
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                                                                                                                                                                                                                                                                          ischaemia;
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                                                                                                Asai S,
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                                                                                                                                                                                                                                                                                                              condition related
                                                                                                                                                                                                                                                                                     compressive ischaemia;
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89.4%;
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          group comprising these
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RESULT 3
AAK83782/c
ID AAK837
XX AAK837
XX AAK837
XX Human;
XX Human;
XW Cytost
XX Homo s
PN WO2001
XX Homo s
YX Homo s
PN WO2001
XX 17-JAN
XX 17-JAN
XX 17-JAN
PR 04-FEB
PR 04-FEB
PR 11-MAR
PR 11-MAR
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                                                                          10-MAR-2000;
11-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2754
                          26-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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  2000US-0214886.

2000US-0215135.

2000US-0216447.

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            CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnossis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cx expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent. (CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 co AAK87694 represent human immune/haematopoietic antigen genomic conservations.
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11-AUG-2000;
11-APR-2001;
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                                                                 proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
                                     ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 at ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL
                                                                                                                                                     The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
                                                                                                                                                                                                                                                      An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothel marker (TEM) protein, useful for inhibiting tumor growth - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytost. normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; necangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthri
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; 2000US-224360P.
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65.3%;
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Best Local
                                                       immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
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Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Parkheimer's; Parkhison's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokinetic;
leukaemia; ss.
utilisation of the activities such as: Immune systematrin/inhibin activity, chemotactic/chemokinetic
                                         lateral sclerosis, and Shy-Drager Syndrome. Other uses include
                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                              Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2000;
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19-OCT-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI60019 standard;
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QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                      SEQ ID
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2000US-0553317.
2000US-0558042.
2000US-0623312.
2000US-0653450.
2000US-0653450.
2000US-06539356.
2000US-06939365.
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Wehrman
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system injurio
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Xu C,
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Pred. No. 1.
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Mismatches
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Xue
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                  Immune system suppression
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Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       λ, A
RX
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Zhang
                                                                                                                                                                                                                                                                                                                                       disorders
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RESULT 6
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ID AAK75883;
XX AAK75883;
XX AAK75883;
XX DT 07-NOV-2001 (first of the content of the conte
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Best Local S
Matches 45
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Note: The sequence data for this patent did not form part of the printed specification.
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cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2001 (first entry)
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45; Conservative
 2000US-0186350.
2000US-019874.
2000US-0190076.
2000US-0199153.
2000US-02014886.
2000US-02116847.
2000US-0216847.
2000US-0216847.
2000US-021880.
2000US-021829.
2000US-021829.
2000US-021829.
2000US-022964.
2000US-022964.
2000US-0225213.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225276.
2000US-0225276.
2000US-02252777.
2000US-0225777.
2000US-0225779.
2000US-0225779.
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2000US-0180628
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Pred. No. 1.9;
0; Mismatches
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08-SEP-2000;
12-SEP-2000;
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22-AUG-2000
23-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
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01-SEP-2000
05-SEP-2000
05-SEP-2000
06-SEP-2000
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2000US -0226681
2000US -0227688
2000US -0227182
2000US -0229343
2000US -0229287
2000US -0229287
2000US -0229287
2000US -0229513
2000US -0229513
2000US -0221443
2000US -0231244
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2000US -0231243
2000US -0231241
2000US -0231241
2000US -0231241
2000US -02323063
2000US -02323081
2000US -0232401
2000US -02346474
2000US -02346474
2000US -02346476
2000US -0246476
2000US -0246675
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2000US -02466524
2000US -02466524
2000US -02466524
2000US -02466610
2000US -02466113
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                                                                                                                                                AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK64950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                             Best
                                                             Matches
                                                                                          Query Match
46144 CAGCCCGGACCTCCAGGTGACCAGGGTCCTCCTGGAATTCCAGGGCAGCCAGGATTTATA 46085
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05-DEC-2000;
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11-DEC-
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17-NOV-2000;
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                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ( HUMA - )
                13 CACCCCAGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGTTTACCACAATATATACA 72
                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA,
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME
                                                                                                                         51935 BP; 14418 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249207
2000US-0249210
2000US-0249210
2000US-0249211
2000US-0249213
2000US-0249213
2000US-0249214
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249244
2000US-0249244
2000US-0249265
2000US-0249265
2000US-0249265
2000US-0249265
2000US-0249269
2000US-0251930
2000US-0251030
2000US-02511856
2000US-02511856
2000US-02511868
                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NO 30695; 3071pp +
                                                                            38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human immune/hematopoietic antigen polypeptides diagnosing and/or treating cancers and
                                                                                                                       12317 C; 11675 G; 13525 T; 0 other;
                                                             0;
                                                                            Score 31.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing; English
                                                                            .2
                                                                                            ĎВ
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                                                                                         Length 51935;
                                                             Indels
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                  Query Match
Best Local
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2000;
30-JAN-2001;
15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46084 GGCGAAAT 46077
                                                                                                                                                                                                                      stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the polynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosts, prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the development of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays. ARK4460-ARK4209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-241741/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001; 2001WO-US24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK44109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK44109
                                                                                                                                                                               Sequence 549 BP; 122 A; 167 C; 137 G; 119 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                        sequences encoding human pancreatic tumour proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 126; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding pancreatic tumour polypeptides, useful pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyle RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA #49 encoding human pancreatic tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2002
                                                                                                                                                                                                           represent cDNA sequences encoding for human pancreatic tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200212331-A2
466
                                                           406
                            61 CCACAATATACAGGAGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                      1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCCTCCTGGTGCACCAGGTTTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGAAAT
CCAGGACCTCCTGGNGCTATA
                                                           GGATCTCCAGGATACCAAGGACCCCCTGGTGAACCTGGGCAAGCTGGTCCTTCAGGCCCT 465
                                                                                                                    1 Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic tumour protein; immune response;
pment of cancer; cancer progression; cytosta
                                                                                                                                                                                                                                                                                                                                                                                                                      ent invention relates to the isolation of cDNA sequences human pancreatic tumour proteins. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-223130P.
; 2001US-265447P.
; 2001US-291201P.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA; 549
                                                                                                                                37.5%;
60.5%;
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486
                             81
                                                                                                                    0;
                                                                                                                                  Score 30.4; D
Pred. No. 1.8;
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                                                                                                                    Mismatches
                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 esponse; pancreatic cancer; cytostatic; gene; ss.
                                                                                                                    32;
                                                                                                                                                 Length
                                                                                                                     Indels
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RESULT 8
AAH48067
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AAT84 484
ID AAT8
AC AAT8
XX 19-1
XX Huma
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XX CX Homx
XX CX Homx
XX CX Homx
XX US5
FT CDS
FT US5
XX US5
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for preparing a protein which interacts with the heat shock protein HSP47. The method involves the two-hybrid screening method using the HSP47 gene and a mammalian CDNA library. The present sequence is the coding sequence for a murine HSP47 interacting protein which was used in the present method. The HSP47 interacting proteins are useful for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine;
                                                                                                                                                                                                                                                            Alpha-1 collagen;
                                                                                                                                                                                                                                                                                                                Human alpha-1
                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page 18-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Using the two-hybrid screening method to prepare proteins which interact with the heat shock protein HSP47 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2001145493-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine HSP47 interacting protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH48067 standard; cDNA; 1317
  01-JUL-1997
                                                   US5643783-A
                                                                                                                                                                                                                                                                                                                                                                                                                      AAT84484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT84484 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1317 BP; 275 A; 422 C; 410 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1999;
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                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAGA-) KAGAKU GIJUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCACG 56
                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCACCGGGGCCACGCGGGCTCCCTGGAGAGATGGGGCGCCCTGGTCCACCAGG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG64211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                collagen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0330631
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                                                                                                                              Location/Qualifiers
1..2055
                                                                                                                                                                                                                                                            type XVIII collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an increase or decrease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHINKO JIGYODAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.4; Di
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                            cartilage degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in activity of HSP47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 10
AAX78379
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A cDNA clone (AAT84484) codes for a human novel type alpha-1 (XVIII) collagen (AAN26327) that is expressed in multiple tissues, especially liver, lung and kidney. It was isolated from a placental cDNA library using a probe based on an unidentified collagenous protein and a probe based on mouse alpha-1 cDNA clone mc19. A claimed plasmid comprising alpha-1 collagen nucleic acid and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The collagen may be used to treat a patient suffering from a disease associated with degradation of cartilage, and for supplementing
                                                                                                                                                              CDS
                                                                                                                                                                                                                                     Alphal(XVIII) collagen; mimetic; endostatin; atomic coordinate; library; anti-angiogenic; heparin binding domain; receptor binding domain; mimic; alpha-helix A domain; carbohydrate recognition domain; CRD domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               앍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 23-30;
                       16-DEC-1997;
                                                                                                                                                                                                                                                                                         Human alphal (XVIII) collagen cDNA.
                                                                                                                                                                                                                                                                                                                                           AAX78379;
                                                                                                                                                                                                                                                                                                                                                                    AAX78379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3394 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding human alpha-1 collagen recombinant alpha-1 collagen, for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-350247/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1993;
                                              16-DEC-1998;
                                                                        24-JUN-1999
                                                                                                WO9931616-A1
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                         treatment; angiogenesis; tumour; human; ss
                                                                                                                                                                                                                                                                                                                    25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                  670
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCCTCCAGGACCCAAGGGCCCCAAAGGAGAAGTGGGCCCCCCCGGACCACCAGG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen BR
                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                  (first
                       97US-0069727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0159784
                                               98WO-US26783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9305-0159784
                                                                                                                       /*tag= a
/product= "alphal(XVIII)
/note= "Partial sequence,
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 668 A; 1130 C; 1080 G;
                                                                                                                                                                                                                                                                                                                                                                    cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.4;
Pred. No. 2
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                                                                                                                         collagen", no start
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cartilage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3394;
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(HARD ) HARVARD COLLEGE

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RESULT 11
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Best Local (
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Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a pinvolves detecting the level of expression of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain, and a carbohydrate recognition domain (CRD) domain. The methods can be used for designing and selecting endostatin mimics. The compounds identified can be used for treating undesired angiogenesis, e.g. tumours. This sequence encodes human alphal(XVIII) collagen which is used in the
                                                                                                                                                                                                                                                                                                                              02-OCT-2001; 2001WO-US30589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
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                                                                                                                                                               Horne
                                                                                                                                                                                                                      (GENE-)
                                                                                                                                                                                                                                                                         02-OCT-2000;
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                                                                                                                                                                                                                      GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               progression;
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                                                                                                                                                                                                                      INC
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71.4%;
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                                                                                                                                                                 Peres-Da-Silva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki
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Pred. No. 2
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                                                                                                                                                               Vockley
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o or more
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity due to the control of the 
                                                              Claim 1;
                                                                                                                             Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tomato; monkey; dog; sea urchin; expressed sequence tag; Es diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatocellular carcinoma in a patient, involving detecting the level expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           progression of liver cancer, hepatocellular carcinoma or metastatic litumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of the patient of the level of
                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                    Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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40; Conserv
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Drmanac RA,
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2000US-0663870
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                                                       314-315; 1275pp;
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RA, Zhang
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J, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                      The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; qene therapy: nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide antibodies and resear
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DB; AAM23752.
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                                                                                                                                                                                                                                                                                                                                                                         Page 381-382; 1275pp;
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2000US-0617746.
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A, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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an T;
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Sequences AAS44576-AAS44919 represent full-length polynucleotides contig polynucleotides encoding polypeptides of the invention. The and protein sequences are useful for the treatment, diagnosis and

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prevention of various types human, dog, monkey, mouse, l such as leukaemia, lymphoma

hamster or rat. The a and neuroblastoma,

of disorder in a mammalian subject su hamster or rat. The disorders include

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18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
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                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antinflammatory;
                                                                                                  Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays
                                                                                           detection
                                                                                                                                                                                               Tang
                                                                                                                                                                                                                                                                                                   26-FEB-2001;
                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
neuroprotective; osteopathic; antidiabetic; antiasthmatic; anti
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DB; AAU27990.
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Yang
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2000US-0577409.
2000US-0597707.
2000US-0616807.
2000US-0664641.
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Pred. No. 3.8;
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Ma Y,
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RESULT 1:
AAS27013
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Matches
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07-JUN-2000

28-JUN-2000

30-JUN-2000

30-JUN-2000

30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatold arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzhelmer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss;
                                                                                                                                                                                                                                                                                                                                               Homo
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   2000US-0179065.

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11-JUL-2000
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14-AUG-2000
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2000US-0232081
2000US-02323081
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2000US-0239935.
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20-OCT-2000
01-NOV-2000
08-NOV-2000
The invention relates to novel isolated polypeptides (I), and polypucleotides (II). (II) (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative
                                                                                                                                                                                                                                                                                   08-DEC-
                                                                                                              Claim 1;
                                                                                                                                   Novel polypeptides useful for diagnosing, prognosing disorders related to the protein disorders and neuronal disorders -
                                                                                                                                     disorders
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DB; AAU17096.
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                                                                                                            SEQ ID No 48; 880pp; English.
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2000US-0254097.
2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention.
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CTGCACCAGGCTGACGGA 1382
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Search completed: February 19, 2003, Job time: 65.0336 secs 22:56:13

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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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LOCUS	HS302D9 145880 bp DNA: linear PRI 12-DEC-1999
DEFINITION	Human DNA sequence from clone RP1-302D9 on chromosome 22 Contains
	GSSs, complete sequence.
ACCESSION	Z82198 .
VERSION	Z82198.2 GI:6572207
KEYWORDS	HTG.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</pre>
REFERENCE	1 (bases 1 to 145880)
AUTHORS	Bridgeman, A.
TITLE	Direct Submission

Pred. No. is the number of results predicted by chance to have a

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted CB10 1SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Dec 13, 1999 this sequence version replaced gi:3164067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insertend of clone CTA-282F2 is at 69682 end of clone CTA-415G2 is at 55167 Location/Qualifiers
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                                                                                                                                                                                                       3344. 3652
/note="AluY repeat: matches 1. .309 of consensus"
3653. .3928
                                                                                             /note="MLT1E repeat: matches
5073. .5176
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572. .759
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246. .571
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3929. .4278
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3344. .3652
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/note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-1"
188. .245
                                                                                                                                 /note="THE1B repeat: matches 3.
4279. .4485
                                                                                                                                                                                                                                                                                  /note="AluSq repeat: matches 2.
3323. .3343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/chromosome="22"
                                       /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                           note="L2"
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     matches
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     2579.
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8914..9
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6686. 6987
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13331. .13397
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/note="match: GSS: Em:B56592"
                                       15669.
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13398. .13698
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/note="match: GSS:
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10718. .11310
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15669. .15727
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14368. .14452
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14061. .14367
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/note="AluSx repeat:
                                                                                           'note="MLT1B repeat:
                                                                                                                             note="L2 repeat: matches 2112.
                                                                                                                                                                                                       note="match: GSS:
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l3806. .13919
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'note="FAM repeat: matches 3.
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                    repeat: matches 119.
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                                                                                                                                                                                                                                                                                                                                                                                          matches 24.
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 Direct Submission
Submitted (13-NOV-2001) De Maere V.,
Shent, Salisburylaan 133, 9820 Merell
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                57;
                                                       De
                                                                                                      De Maere, V., Vercauteren, I., Claerebout, E. Identification of potential protective ant
                                                                                               probes
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Maere, V.
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23905. .239
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16028. .16245
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                                                                   1 to 287)
                                                                                                                                                                                                                                                                                                                                                                                                                 'note="MER66-internal repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER66-internal repeat: matches 1210. .2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSp repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="THE1B repeat:
22302. .22537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
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/note="77 copies 2 mer tt 70 conserved"
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                  Merelbeke,
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                  Parasitology,
beke, BELGIUM
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Hydra sp.
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                                                                                                                                                                                                                                                                       See
                                                                                                                                                                                                                                                                                                          Kurz,E.M., Holstein,T.W., Petri,B.M., Engel,J. Mini-collagens in hydra nematocytes J. Cell Biol. 115 (4), 1159-1169 (1991)
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JUL-1991)
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/clone_lib="lambda gt10,
14..676
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/db_xref="taxon:6317"
1. .287
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/clone="3, 2/55"
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<1. .>287
                                                                                           /gene="N-COL 1"
                                                                                                                                 /gene="N-COL 1"
                                                                                                                                                      /gene="N-COL 1"
                                                                                                                                                                                                                     /strain="SF1
                                                                                                                                                                                                                                 ∕organism≕"Hydra sp.
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                             /codon_start=1
                                                                                                                  /evidence=experimental
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2; Mismatches
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David, C.N.

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                                                                                                                                                                                                                                                                                                                             Submitted (03-MAR-1994) Pascal P J-M Chareyre, (
Universite Claude Bernard Lyon, I, 43, Bd du 11
VILLEURBANNE, 69622, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chareyre, P., Besson, M.T., Fourche, J. and Bosquet, G. Identification of a Bombyx collagenous protein with multiple short domains of Gly-Naa-Yaa repeats: CDNA characterization and regulation of expression
                                                                                                                                                                                                                                                                                                                                                                                   Chareyre, P.P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidae; Bombycidae; Bombyx.

1. (bases 1 to 1993)
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                                       /note="pro
248. .373
             PGQPGQPGYPGQGGPQQGGQPMNPSQPGYPGQPGQPGQPGQPFGTPGQAGHPGQPGHPGAP
QPGTPGQPGYPGQGGPQQGGQPMNPSQPGYPGQPGQPGQPGQPGQPGTPGAPG
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/tissue_type="Imaginal wing disc"
/clone_lib="Lambda gt10 cDNA library"
/dev_stage="Vth instar"
<1...1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="N-COL 1"
/gene="N-COL 1"
/note="collagen-like region"
/note="collagen-like region"
/note="123 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="mini-collagen" 167. .235
<u>GQPGYPGQPGQPGAPGQAGYPGQGGPQQGGQPINPSQPGHPGQPGQPGQPGQPGKPGC</u>
                                                                                                                                                                                                                                                /organism="Bombyx mori"
/strain="European 200x300"
/db_xref="taxon:7091"
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74. .460
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Saimiriine herpesvirus 2.
Saimiriine herpesvirus 2
Saimiriine herpesvirus 2
Viruses; dsDNA viruse; no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fickenscher, H., Bokel, C., Knappe, A., Biesinger, B., Meinl, E., Fleischer, B., Fleckenstein, B. and Broker, B. H., Fleischer, B., Fleckenstein, B. and Broker, B. T. fleckenstein, B. and Broker, B. J. fleckenstein, B. J. flec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Virol.
97184558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1996) H. Fickenscher, Universitaet Erlangen-Nuernberg, Institut fuer Klinische und Molekulare Virologie, Schlossgarten 4, D-91054 Erlangen, FRG (bases 1 to 3734)
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                                                                                                                                                                                                complement(473. .1270)
/gene="TipC484"
/codon_start=1
                                                                                                                                                                                                                                                                                                                            /lab_host="Owl monkey kidney cells"
/note="this strain is different from strain C484
database entry M31964; transformation-associated
complement(473] .1270)
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/db_xref="GI:1743283"
/db_xref="GI:1743283"
/translation="MANEGEEIELTEFPETEKERKDEEKLSSCSEETTDTSSSSSSDH
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VPAPIEVNVIIQNSSRTEDELQNSTKFAVANEGKEIELTGFQGKLSSCSEETTATSSS
YSSKQASVCIEENGDNETSTYRPQNVLTNLNSLYTTFEDARAQGKGMVRYKSEDLQSF
                                                                                                                                                                                                                                                                                          /gene="TipC484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /specific_host="Saimiri sciureus"
/sub_species="subgroup C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C484"
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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Phahditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NOTICE:
                                                                                                                                                                                                                                                                    waterston, R.
                                                                                                                                                                                                                                                                                                The sequence of C. elegans cosmid EGAP7
Unpublished (2001)
3 (bases 1 to 6522)
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49; Conserv
                                                                                                                                         Louis, MO 631
Submitted by:
                                                                                                                                                                    Submitted (22-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                  Submitted (19-MAY-1996) Robert Waterston 4 (bases 1 to 6522)
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                                         Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.a
: This sequence may not be the entire insert of this clone be shorter because we only sequence overlapping sections
                                                                                                                                                                                                     Submission
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/gene="StpC484"
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/db_xref="GI:1743282"
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KANERNIVKDLKRLENKVNAIICLVVVILAVLLLVTVLSILHIGMKS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                              jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3734;
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

For a graphical representation of this cosmid analysis see: http://www.wormbase.org/db/seq/sequence?name=EGAP7;class=Sequence sequence and its

## NEIGHBORING COSMID INFORMATION

The 5' cosmid is F53B1, 200 bp overlap; the 3' cosmid is F48B9,

## NOTES:

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE\_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964). /db\_xref="taxon:6239" /organism="Caenorhabditis elegans" /strain="Bristol N2" Location/Qualifiers

ORIGIN BASE COUNT FEATURES gene CDS source 2260 PRGPPGQPGSCDHCPPPRTGPGYARR" 998 c 1175 g 2089 t GSCCTCQVGPPGPPGPPGRDGRPGAPGRPGNPGPPGRDGALLPGPPPKPPCQKCPPGP PGPAGPPGPKGLPGPQGDAGTSGQDGVPGLPGPPGPSGPQGAPGVPGEKGPTGEPGKV /translation="meokcaprrslrulaiasatlaivsmlatviivplvynhvqhlq Svmnsevdfcktrsrdlwremvtvqsatggipartarrtrrdnygaqpiaanpessaa complement(join(4209. .4952,5035.
/gene="EGAP7.1" **INGAPPGPPGPPGPQGPPGPPGKDGQPGKAGPPGLPGDPGEKGSDGLPGPHGGTG** /product="Hypothetical protein EGAP7.1"
/protein\_id="AAB00598.1"
/db\_xref="GI:1326298"
/db\_xref="GI:1326298" /note-"coded for by the following C. elegans yk289e5.3, yk327f2.3, yk327f2.5, yk289e5.5" -Sequence" /note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=EGAP7.1;class complement(4209. /gene="EGAP7.1" /clone="EGAP7" codon\_start=1/ /chromosome="> .5199) .5199)) cDNAs:

Q Вb Qy Query Match Best Local Matches 4787 61 CCACAATATACAGGA 75 1 GGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 49; Similarity Conservative 41.2%; 0; Score 33.4; Pred. No. 2; Mismatches B 26; Length Indels 6522; 0 Gaps 60

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or longer because we provide a small overlap between

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone F57B1. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                             the specified clone. It may be shorter because we only overlapping sections once, or longer because we arrange overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions.

The true left end of clone F57B1 is at 1 in this sequence. The true right end of clone F57B1 is at 5273 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-AUG-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predictions from Genefinder (P. Green, U. Washington),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence Z78060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The C.elegans Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences below are predicted from computer analysis, using
                                                                                                                                                      /gene="F57Bl.2"
complement(join(3851...41.4921...5024,5071...5452))
                                                                                                                                                                                                                      complement(join(3851. .41
4921. .5024,5071. .5452))
/gene="F57B1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            left end of clone C34D1 is at 35789 in this sequence. The this sequence (1. .104) overlaps with the end of sequence
                                                                   /note="predicted using Genefinder cDNA EST yk669g9.3 comes from thi cDNA EST yk669g9.5 comes from thi
/protein_id="CAB01511.1"
/db_xref="GI:3877753"
                                                 /codon_start=
                                                                                                                                                 /gene="F57B1.2"
                                                                                                                                                                                                                                                                                                  /clone="F57B1"
                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is NOT necessarily the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36532 bp DNA .....cosmid F57B1, complete sequence.
                                                                                                                                                                                               .4162,4210.
                                                                                                                                                                                                                                                                        .4162,4210.
                                                                                                  this
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                                                                                                                                                                                                                                                                     .4629,4674.
                                                                                                                                                                                             .4629,4674. .4877
                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          we arrange
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for a small
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CDNA EST yk33c11.3 comes from this gene cDNA EST yk33c11.3 comes from this gene cDNA EST yk70b10.3 comes from this gene cDNA EST yk102c6.3 comes from this gene cDNA EST yk102c6.3 comes from this gene cDNA EST yk102c6.3 comes from this gene cDNA EST yk99c7.3 comes from this gene cDNA EST yk99c7.3 comes from this gene cDNA EST yk79c11.3 comes from this gene cDNA EST yk70b10.5 comes from this gene cDNA EST yk102c6.5 comes from this gene cDNA EST yk102c6.5 comes from this gene cDNA EST yk102c6.5 comes from this gene cDNA EST yk170f7.3 comes from this gene cDNA EST yk170f7.5 comes from this gene cDNA EST yk170f7.5 comes from this gene cDNA EST yk170f7.5 comes from this gene cDNA EST yk170f7.3 comes from this gene cDNA EST
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/translation="MNNGQYEYDERILMKHYVLSCETSSGIKNIAPPTIVQTIEILIQ
FILPIFILGIYIAIIIKILMKKAALNKYELTILKQAISSSVFLLGQTIKFEIATAFL
IKRINNTEICAGAATPCFFFFTSKEIRKLVSVRVSLTTSQANSNSQQRRQTSRAI"
complement(join(10251...10976,11025...11240))
/gene="F57B1.3"
/gene="F57B1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-value=9.7e-10, N=3; PF01484 (Nematode cuticle collagen N-terminal domain), Score=40.6, E-value=1.1e-08, N=1 cDNA EST yk93c11.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F57B1.4"

complement(join(13023. .13760,13809. .13948,14082. .14274))
/gene="F57B1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(13023.
/gene="F57B1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GADAAVGGFGGSAGGSCCSCGTGAAGPAGSPGQDGAPGNDGAPGAPGNPGQDASEDQT
AGPDSFCFDCPAGPPGPSGAPGQKGPSGAPGVPGQTGGASLPGPPGPAGPPGPSGQPG
SNGNAGAPGAPGQVVDYPGTPGPAGPPGPPAGPPGPAGAPGQPGOSGSGQPGGPGPQGDAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F57B1.3"
/note="predicted using Genefinder
/notes-predicted using Genefinder
contains similarity to Pfam domain: PF01391
triple helix repeat (20 copies)), Score=45.4
E-value=4e-10, N=3; PF01484 (Nematode cuttol
N-terminal domain), Score=40.6, E-value=1.1e
cDNA EST yk73c7.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contains similarity to Pfam domain:
triple helix repeat (20 copies)), Sc
E-value=9.7e-10, N=3; PF01484 (Nemai
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/translation="MSSEDPKQIAYETESLRKVAFFGIAVSTIATLTAIVAVPMLYNY
MQHVQSSLQSEVEFCAHRSNGLWDEYQRFEGVSGVAGRIKRESYHRKARASKVRRQSY
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LIGASIDHSCSSRPVSAKDGFFYDFMSYFGTFQEGYALLDRDVLSPGEAWCTYDKRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MALRHTISPQFSNRHSPPVTRSVSRTGVHQPLDTSTPVTRRDSQFSTTTTGTTQRFHESADDSETDLNSSKFIYKEHFSYKEITSMKKEMMYVPMLEYYIRMVRRRVPTWADFKRTLMAVVLEAMLYKYARDCLFDGTHHINSGSYADKDANWASBKQKFIRMVRQTTSNLRAEFSAHDKOLDFKTDHLEKLLENVLEHSKGWKESAIEELKQIKLWQAEISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGAPGQPGQAGAPGQDGDSGSEGACDHCPPPRTAPGY"
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/db_xref="GI:3877751"
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/translation-"MAEHTGVIDKAVEGGEKPNGSWFEFLASALPYYVLSEYYTLASI
KGMTRQWSNHLTTRSCPFSHFSTIATLTAIVAVPMLYNYMQHVQSSLQSEVEFCAHRS
                                                                                                                                  /protein_id="CAB01508.1"
/db_xref="GI:3877750"
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/db_xref="GI:3877752"
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                                                                                          /db_xref="SPTREMBL:Q20921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder
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                                                                                                                                                                                                                                                                                                                                                                   1 GGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60
                                                                                                                                                                                                                                                                         CCACAATATACAGGAGAA 78
                                                                                                                                                                                                                                                                                                                       GGACCACCAGGGCCCATCAGGAGCCCCCAGGACAAAAGGGACCTTCAGGAGCCCCCAGGAGTC 10617
     Caenorhabditis elegans cosmid AL132952 AL031823 AL132952.1 GI:6434491 HTG:
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                                                                                                   CEY51H4A
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STSPLMTSLPLRLSGFPLLNIRDPSAEASLLNLGCNADAAALLKTILDQYRMLEEASM
SMSSSPSKDDESGDEDSDGLNSNSIIDVITDYPIFCLSRAFVLSNYPRFHPPLHLTLD
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/gene="F57B1.7"
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complement(join(34555. .3469;
/gene="F57B1.7"
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DGDSGSEGACDHCPPPRTAPGY"
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GPSGAPGQKGPSGAPGAPGQSGGASLPGPPGPAGPPGPSGQPGSNGNAGAPGAPGQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:Q20920"
/translation="MADQIKIRRRQRKDTLLTFAKNSITSTMFPSNQISLNALNSLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB01507.1"
/db_xref="GI:3877749"
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AFWLFPSSTFSLILSFLSLLFLSAGPRVIKFAVDNQMILSLAHALLMCGACILSSFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:Q20926"
| translation="MTMNYCGINLKLNYVIDAVQCKLQRSFSAVTLHLCETRLGDSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB01513.1"
/db_xref="GI:3877755"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA EST EMBL:T01341 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24748. .24830,2
/gene="F57B1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24748. .24830,25045. .25267)
/gene="F57B1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB01512.1"
/db_xref="GI:3877754"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(19688. .19768,19816. .19867,19913.
20538. .20687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(19688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGLWDEYQRFEGVSGVAGRIKRESYHRRASGPHRASKVRRQSYGADAAVGGFGGSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )oin(23062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MPGENKFYKYFVVYPFNVLSISKITIILLILSLYGWDTKQRIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q20925"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                               41.0%;
64.1%;
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                                                          269619 bp ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.2;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                   DNA
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••
                                                                          complete
                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 36532;
                                                                                                 linear
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                                                                          sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone Y51H4A. The true left end of clone Y43D4A is at 193825 in this sequence. The start of this sequence (1.115) overlaps with the end of sequence AL713992.

The end of this sequence (269514. .269619) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-OCT-1999) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on May 14, 2001 this sequence version replaced gi:5730145. Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of sequence AL132846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulston, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The C.elegans Sequencing (bases 1 to 269619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 282
99069613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         none
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9851916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           name=Y51H4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(2293. .2346,2393.
3398. .3694,5250. .5357))
/gene="Y51H4A.1"
                                                                                                                                               complement(join(12157. .12228,13962.
17111. .17131))
                                                                                                                                                                                                                         complement(join(12157. 17111. .17131))
                                                                                                                                                                                                                                                                                           LAENSKNLEKSSQSNDPENAEETEMVIELHTEAAPVENYLEEEIQIKVPEVEEDTEKT
PAGSPKSTSSCISSEILSEQSIGTCAKLYCFTNRPTLYGFRHTAEPVCCRVLARPQFQ
NFNCFKFSSISPRPSSFPLDFATSSYSAPLSNFTRETPNIVPRMMSEEFESLHKCIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
                                                                    /note="contains similarity to Pfam dom:
family), Score=317.2, E-value=6.4e-92,
                                                                                                                                                                                                                                                RKSDIRDLLRRIQSAKRRHRRFSEHLQQVQHDHHIDY"
complement(join(12157. .12228,13962. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(2293. .2346,2393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Y51H4A"
                                                                                                                        /gene="Y51H4A.
                                                                                                                                                                                               /gene="Y51H4A
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/db_xref="GI:6434492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3398. .3694,5250. .5357))
/gene="Y51H4A.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .269619
EST yk60d10.5 comes from this gene EST yk103g7.5 comes from this gene EST yk77f3.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consortium
                                                                          domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2610,2668. .2758,
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                                                                                                 PF00071 (Ras
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/gene="Y51H4A.../note="pro2"
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53245. .53366,53557. .53611,54196. .54274,54700. .54854,
55009. .55055,57258. .57575))
/gene="Y51H4A.5"
complement(join(50748. .50898,51588. .51977,52741. .52920,
53245. .53366,53557. .53611,54196. .54274,54700. .54854,
55009. .55005,57258. .57575))
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TALPFFAQHFAPYANPHATSSFSPSSSSTSSTTSSQNQQSGSSGSKKKKPVPVPPENQK
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complement(join(31618. .31755,32295.
33718. .33834))
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/db_xref="SPTREMBL:Q90265"
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VDNGKKMRRRGKAKPILTQFISKSFFLFDKMYKNEVELSYFKSSIFCTFFPKKITPFR
LLGDITAPLKLSVRAAAERERRAATRIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(21593..21756,22186..22384,22466..22675))
/gene="Y51H4A.2"
/codon_start=1
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complement(join(21593. .21756,22186. .22384,22466. .22675);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
CDNA
CDNA
KSLNCPELPDKAHAYDDNFVRTKIVPLAASALNPNPEKCFKPRLPTMTLSKKFSANCS
EVGPQSNCFSFTSFDTTQKVLVMSFRGTDSPLQLTDEILDFFTGKKQFFPDAGNIFTY
FYDAFFFLMNAGLQQDIRQLKYKYPDYELMVTGHSLGGALASVAASYVVHTGIFTSDK
                                                                                                                                                                                                                                                               /note="predicted using Genefinder contains similarity to Pfam domain: Score=244.3, E-value=5.4e-70, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(31618. .31755,32295. 33718. .33834))
                                                                                             /translation="merlnmcQlyLLHLFFLYVCCWIVGTSALGRAEYTCSHEKTINL
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/db_xref="GI:6434495"
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QHLLLQNPGTIDTMDPIAMANMPSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB63379.1"
/db_xref="GI:6580310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Y51H4A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                       /db_xref="SPTREMBL:Q9NAE3"
                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:Q22038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA EST yk340d3.3 comes from this gene NA EST yk479g1.3 comes from this gene NA EST yk282h7.5 comes from this gene NA EST yk340d3.5 comes from this gene NA EST yk479g1.5 comes from this gene NA EST yk479g1.5 comes from this gene NA EST yk573a7.3 comes from this gene NA EST yk573a7.5 comes from this gene
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61 CCACAATATACAGGAGAA 78
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                                                                                                                                                                                                                                                                                                                                                                                  GGACCACCAGGACCATCCGGAGCTCCAGGACAAAAGGGACCTTCAGGAGCACCAGGAGCT 130087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
50; Conserv
Hydra vulgaris
Hydra vulgaris
                                                                      AF282902.1 GI:11875611
                                                                                               complete cds.
AF282902
                                                                                                                                           Hydra vulgaris type IV collagen
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MIAVRNALRY LPKEHHYLLATEFAEELNTYGHIGYGYREWPNFDLFAPPVSEIGAHCEQ
ASAIILMILMILDKRYAGPFOELVTYGGNGOYPSNNIOFRLVLRYLTMTDHOTLULY
SGHPLGLFPSTPDSPRMTVTNGMMIPSYSTKELYDKYFALGVTQYGQMTAGSFCYIGP
OGIVHGTTITVLNAGRRMGLDSLAGKYFVTAGLGGNGGAGPKAKIAGCIGVIAEISD
TALLKHQQGWLDVYSKDLEEIVNMIKEYFEKKEISIGYLGNVVDLWERLAEEPECL
VELGSDQTSLINDFLGGYPAGLTFEGGNQMMTSDPVKFKKLYGNSLTRQIAALDKIA
AKGMYFWDYGNAFLLECQRAGANLLREDAQDDKSFRYPSYMQDIMGDIFSMGFGFFRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Y51H4A.t1"
80385. .80457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCTSGKPEDLRLTDQTACKIIDELKDTDVPEYYKQQYLDNKKWIEEAEKNKLVVGSQA
RILYSDRAGRVALASAFNELVKSGKVSAAIVISRDHHDVSGTDSPFRETSNVYDGSAF
TADMAVQNCIGDSFRGATWVALHNGGGVGWGDVINGGFGIVLDGSSDAARRAEGMLNW
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/gene="Y51H4A.7"
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NNNMSTTEPYHICAEADGFYCSSRELDTNIADHLTYFGVFIPGWQTKC"
join(61826 . 61986,62058. .62127)
/gene="Y51H4A.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVPNGVTRRSWSGNAKAQEAIQRAEKQVDGLRVTLPVEADEELLKKLKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/protein_id="CAB61139.1"
/db_xref="GI:6434497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q9NAE2"
/translation="MQSSDREVVVKDRNLEPEDENHQNREFYGGDLLGGKEHTTWEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB63381.1"
/db_xref="GI:6580312"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.2; DB Pred. No. 3.1; 0; Mismatches
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                                                                                                                                                                   5851 bp
                                                                                                                                           mRNA linear INV 17-DEC alpha 1 chain precursor, mRNA,
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1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterization of hydra type IV collagen. Type IV collagen is essential for head regeneration and its expression is up-regulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      upon exposure to glucose
J. Biol. Chem. 275 (50), 39589-39599 (2000)
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                                                                                 Similarity
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                                                          Conservative
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KQGPPGAEGPQGEKGERG IGTDKGTKGTTGDTGLTGLOGFKGERGERGENGRGDQGP IGP
KQGVPGAEGPQGEKGERG IGTDKGTKGETGDI IGLGGPKGERGERGENGRGDQGP IGP
KGDVGEPGPGASIGNTGI SGNDCPKGESGPPGI KGEPGSVGSI GPKGSKCEQGEKGER
GSTLKGNPGI EGPRGFTGPPGPAGKDY ILDLEVGPLGEKPTKGEPGEDGPKGDKGDI IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKGEPGLKGDPGKPGLDGAPGKSVPKGEPGRDGKDGDPGAKGEPGTPGESGRDGEKGE
IGPQGPQGDKGDQGQSVIGPKGETGAIGKKGETGQDGLKGRDGIGKQGANGEKGEKGN
SVVGLPGDPGEKGSPGEKGKDGISGKQGKPGPPGKDGVDGTPGKDGLPGNPGPEGPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGDPGTDGPQGPQGLQGPQGDRGAPGKSGIPGNNGEKGEKGNKGDGLRGFKGERGR
DGEPGPKGSQGPMGKPGPKGEPFSTALKGQQGDKGDVGSEGPPGPQGAEGQVGNQGFK
GEPGLLGAPGSGEKGEKGDAGTPGIAGKNGENGKDGQDGPKGDKGEKGLQGPIGISGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGPEGPKGDSGQKGETGLDGPKGEKGQPAIGTGPKGEKGDQGPPGPQGPQGDIGEKG
DIGPPGETGDIGPQGIKGEFGIAGIKGETGPPGLQGPIGLKGDQGPPGDAGKVGPPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGMDGNPGQ1GPPGEPG1PGFPGPPGNPGQVVNDLGETVLPGPPGDQGPQG1QGVÄGP
QGSPG1RGDKGDACKSCPSGPQGEKGVAGQDGLPGANGEKGDKGDEGKPGLEGSVGDP
                                                                                                                                                                                                                                                                                                                                                                                                /note="Reg
277. .4641
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DRGEKGEAGQRGYKGEPGPSSQLTINPGAKGEQGDRGIKGEKGNIGPKGINGPFGKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GESGLTGPQGPIGEKGDTGAKGNKGERGSDRIVQGERGEKGTDGMPGSPGSIGFKGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGLKGLKGEIGMTGPSGEPGKTGAEGMKGPIGPAGQRGETGSKGESGRPGQSVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEAGQDGQKGEKGDKGEIGSAGPSGIQGEKGDIGATGAAGTKGEPGSDGSLGSPGQKG
                                                                                                                                                                                             /note="Region: non-collagenous
942 c 1638 g 1318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECHGRGTCWYYGPTLSFWLSTIGESNMFQVPKFEILERNLKARVSRCAVCMKSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSTMPFLFCDIQNKCVVASRNDYSFWLSTAEKPKEAPSSGADLENYISRCIVCEAPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSGDFGFYLVKHSQSIKVPSCPAGMQTMWEGYSFLYAQGNERAFGQDLGQPGSCLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGSQGTKGEKGVPGSKGEKGEQGLEGPKGLEGRVGLAGSKGDKGIKGVIGKPGPTGD
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                                                                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                                                                               /note="N-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                   /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSHGRPGDEGRQGEPGLPGCNGTKGDIGPPGPRGKDGVQGPSGLPGPIGPPGEPGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="type IV collagen alpha 1 chain precursor"
/protein_id="AAG40729.1"
/db_xref="GI:11875612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hydra vulgaris"
/db_xref="taxon:6087"
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                                                                                 40.7%;
                                                                                                                                                                                                                                                                                                                                                                Region: contains collagenous domain"
                                                                                                                                                                                                                                                                                                                                                                                                                        Region: non-collagenous domain
                                                       0;
                                                                                 Score 33;
Pred. No.
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                                                       Mismatches
                                                                                                           DB 3;
                                                                                 .6
                                                       30;
                                                                                                           Length 5851;
                                                                                                                                                                                                                          domain'
                                                       Indels
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                                                    Gaps
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                                                484
61 CCACAATATACAGGAGAAA 79
                                                                                                                            Local
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                                                                            1 GGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCCTCCTGGTGCACCAGGTTTA 60
                                                GGAGCACCAGGATTCCCTGGACGCCCTGGAGTCCAAGGACCTCCAGGGGAACGAGGTTTG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACAATATACAGGAGAAATA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kania,A.M., Reichenberger,E., Baur,S.T., Karimbux,N.Y.,
Kania,A.M., Reichenberger,E., Baur,S.T., Karimbux,N.Y.,
Taylor,R.W., Olsen,B.R. and Nishimura,I.
Structural variation of type XII collagen at its carboxyl-terminal
NCI domain generated by tissue-specific alternative splicing
J. Biol. Chem. 274 (31), 22053-22059 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-MAY-1996) A.M. Kania, Periodontology, Harvard Dental, 188 Longwood Ave., Boston, MA 02115, USA On Sep 12, 1996 this sequence version replaced gi:1518602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus collagen XII alpha U57362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kania, A.M.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collagen
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                                                                                                                           Similarity
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                                                                                                                                                                                          472
                                                                                                            Conservative
                                                                                                                                                                                          a
                                                                                                                                                                                          GGAPGEPGRPGVGGPPGERGLPGEKGERGIGSQGPRGPPGPPGPGGESRTGPPGSTGS
RGPPGPPGRPGNSGIRGPPGPPGPCDCSSQCASIFYNGQGYPEPYVPEGGAYLPDREPF
IVPVEPERTAEYEDDYGADEPEQQHPDHRRWRRALRPGPGQ"

437 c 479 g 388 t
                                                                                                                                                                                                                                                                                  MRAVARQVCEQLISGQMSRFNQMLNQIPNDYHSNRNQPGPPGPPGPPGAAGARGEPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/strain="CD"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                  /gene="Coll2a1"
/note="Col2, NC2, Col1, NC1 domains"
                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Col12a1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="AK#M"
                                                                                                                            40.2%;
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Rodentia;
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                                                                                                            Score 32.6; D
Pred. No. 3.3;
0; Mismatches
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MEDLINE
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  sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clones completing the nucleotide and derived amino acid sequence of the alpha 1 chain of basement membrane (type IV) collagen from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse mRNA for basement x06777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See M12879 for genomic exon 14 sequence with differences shows interrupted GlyXY nature of collagen alpha chain. Described (02-SEP-1988) by Wood L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See M1402 for overlapping sequence (cDNA clone pCIV-1-225, same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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Mammalia; Eutheria;
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od,L., Theriault,N. and Vogeli,G.
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                                                                                                                                      PGSQQVPGSPGEKGAKGEKGQSGLPGIGIPGRRGDKGDQGLAGFPGSPGEKGEKGSAG
TPGMRGSPGPRGSPGNIGHPGSPGLPGEKGDKGLPGLDGVPGVKGEAGLPGTPGPTGP
AGQKGEPG"
151. .231
232. .882
                                                                                                                                                                                                                                                                                                                                              EILGHVPGTLLKGERGFPGIPGMPGLPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKG
QMGSSFQGFKGDKGEQGVSGPPGVPGQAQVKEKGDFAPTGEKGQKGEPGFPGVPGYPGY
KGEPGKQGPRGKPGKDGEKGERGSPGIPGDSGYPGLPGRQGPSGEKGEAGLPGPPGTV
                                                                                                                                                                                                                                                             KGQKGERGLPGLQGVIGFPGMQGPEGPHGPPGQKGDAGEPGLPGTKGTRGPPGAAGYP
GNPGLPGIPGQDGPPGPPGIPGCNGTKGERGPLGPPGLPGFSGNPGPPGLPGMKGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="pCIV-1-PE12, pCIV-1-PE16"
/clone_lib="PYS cDNA"
75. .76
                                                                                                     TPGVPGKDGHAGHPGQPGPKGDPGLSGTPGSPGLPGPKGSVGGMGLPGSPGEKGVPGI
                                                                                                                        GPRGDPGFKGDKGDVGLPGMPGSMEHVDMGSMKGQKGDQGEKGQIGPTGDKGSRGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA29946.1"
/db_xref="GI:50502"
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151. .>3612
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:P02463"
/translation="MGPRLSVWLLLLFAALLLHEERSRAPAKGDCGGSGCGKCDCHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="MGD:MGI:88454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="collagen alpha chain precursor (AA -27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="c was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /citation=[1
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/db_xref="taxon:10090"
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                                                                     DEFINITION
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Best Local
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                                                                                                                                                                                    61 CCACAATATACAGGAGAAAT 80
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J04694
J04694.1 GI:556296
alpha-1 type IV collagen.
Mus musculus 13.5 day old embryo parietal endodoerm
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50; Conserv
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Patent: WO 0188188-A 932 22-NOV-2001;
School Juridical Person Nihon University
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Eukaryota; Metazoa;
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3475. 3555
7/note="exon 4 region"
1011 c 1212 g 570 t
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883. .921
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181
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232. .276
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1798 c 1950 g 1
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A, complete cds.
              CDNA to mRNA
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The complete primary structure for the alpha 1 chain of mouse collagen IV. Differential evolution of collagen IV domains
J. Biol. Chem. 264 (11), 6310-6317 (1989)
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                               /note="|
5777...
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GPRGDPGFKGDKGDVGLPGMPGSMEHVDMGSWGQKGDQGEKQGIGPTGKGSKGFGF
GPRGDPGKDKGDKGLPGMPGSMEHVDMGSWGQKGDQGEKQGIGPTGKGSKGFGF
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                                                                                                                 /note="putative" 5765. .5770
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KGEPGKQGPRGKPGKDGEKGERGSPGTPGDGSGYPGLPGRGKQGPGEKGEAGLPGPPGTV
IGTMPLGEKGDGKYPGAPGLRGEPGFRGFPGTPGQPGPFTPTGQAGAPGFPGEPG
KGDQGFPGVSLPGPSGRDGAPGPPGPPGPPGPCHTNGTVECQPGPPGDQGPPGTPGQ
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GNPGLPGIPGQDGPPGPPGIPGCNGTKGERGPLGPPGLPGFSGNPGPPGLPGMKGDPG
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APFIECHGRGTCNYYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="alpha-1 type IV collagen"
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                                                                            /gene="Col4a-1"
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/dev_stage="13.5 day old embryo"
/gene="Col4a-1"
                                                                                                                                                                 'gene="Col4a-1"
                                                                                                                                                                                                                 'note-"putative"
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5406. .5411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1514)
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-MAR-1998) Laine A., I U377, Place de Verdun, 59045 Lille
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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1798 c 195
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                                                                                                                                                                                                                                                 /gene="MUC5B"
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/gene="MUC5B" /number=21 /number=21 96109720 /gene="MUC5B"	93739511 /gene="MUC5B" /number=21 /5129609	/number=20 89809372 /gene="MUC5B"	/gene=_mucsb /number=19 88288979 /gene="MUC5B"	. 6	81578503 /gene="MUC5B" /number=18 85048604	/number=1/ 81018156 /gene="MUC5B" /number=18	/number=17 75788100 /gene="MUC5B"	/number=16 73227577 /gene="MUC5B"	70807321 /gene="MUC5B"	69537079 /gene="MUC5B"	6855 .6952 /gene="MUC5B" /number=15	/number=14 67606854 /gene="MUC5B" /number=15	/Humber - 14 64706759 /gene="MUC5B"	/Idiliber=13 63086469 /gene="MUC5B"	/Hulliber = 13 5870 6307 /gene="MUC58"	/number=12 57325869 /gene="MUC5B"	/number=12 53135731 /qene="MUC5B"	/number=11 52435312 /gene="MUC5B"	/number=11 49065242 /gene="MUC5B"	/number=10 47954905 /gene="MICSR"	/gene="MUC5B" /number=10 44504794 /gene="MUC5B"

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RESULT 15
HSS171M_3
WPCOMMENT

    Sequence split into 4 fragments
    LOCUS HSS171M Accession AJ239326

    Fragment Name
    Begin
    End

    HSS171M_0
    1 10000

    HSS171M_1
    100001
    210000

    HSS171M_2
    200001
    310000

    HSS171M_3
    300001
    400516

    Continuation (4 of 4) of HSS171M from base 300001 (AJ239326 Homo sapiens chromosome 21

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                                                                                                                                                                                                                                                      Query Match 39.5%; Score 32; DB 2; Length 100516; Best Local Similarity 65.3%; Pred. No. 7.1; Matches 47; Conservative 0; Mismatches 25; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.5%; Score 32; DB 9; Length 15143; Best Local Similarity 79.2%; Pred. No. 6.1; Matches 38; Conservative 0; Mismatches 10; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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396
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1 (bases 1 to 499)
1 (con, D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R., Sun,S.S. and Cheong,I.C.
Sun,S.S. and Cheong,I.C.
Gene Expression Profiling of the Bovine skeletal muscle Unpublished (2002)
Contact: Dr. Du-Hak Yoon
Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Omockchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1792
Fax: 82 31 290 1792
                                                                                                                                                                                                                                                                                                                                                             MM967732 499 bp mRNA linear EST 20-MAR-200 LM24HW0134 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone LM-24-HW-011-34 (5'), mRNA sequence.
BM967732
                                  Email: dhyoon@rda.go.kr
Insert Length: 499 Std Error:
Seg primer: CAGGAAACAGCTATGAC
POLYA-NO.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
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AG080755 Pan trog1
AG080765 Pan trog1
BE729966 601562450
AG052122 Pan trog1
BE728927 601562364
BE728927 601562343
BE728912 60168725
BF304683 601868725
BF304683 601888096
BQ422247 AGENCOURT
AA711635 zg52e04.s
AG014562 Homo sap1
AW898344 RC3-NN007
AQ665181 HS\_5344\_B
B78843 CIT-HSP-734

AQ393565 CITBI-E1-

Bovoidea;

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RESULT 2
BE757275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE757275
211668 MARC
BE757275
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca.
v0.980904.e. Vector identified by
                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                         Contact: Smith TPL
                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                     Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G. Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 504)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: skeletal muscle; Vector: Uni-ZAPXR;
ECORI; Site_2: Xho I"
139 c 131 g 100 t
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/clone_lib="Bos taurus LM-24-HW cDNA library"
/sex="six males mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="longissimus dorsi"
/cell_type="myocyte"
/dev_stage="24 months old"
/lab_host="XL1-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 bp mRNA linear 2BOV Bos taurus cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 105;
called and alt_trimmed with phred by cross_match with the -minscor
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    -minscore
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Best Local S
Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCGTCCCTGGTGTGTACCACTTTGGCTTTGACATTGAGTTGTTTCAGAGTGCTGTCAA
                                                                                          Contact: Smith TPL USDA, ARS, US Meat Animal R PO Box 166, Clay Center, NE Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                           1 (bases 1 to 526)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE757276
211669 MARC
BE757276
BE757276.1
                                  Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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-minmatch 12 options
PRimers
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sa Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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Pred. No. 1.1e-10;
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                                                                                                                              NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 CACAGGGGTCCTGTACAATGCCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTGCTTG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCCTTTCCTTTCAAGCCCATCATCTT 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCGTCCCTGGTGTACCACTTTGGCTTTGACATTGAGTTGTTTCAGAGTGCTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGGAAGTTCTGTACAACCATCAGGGCCACTTCGACCCCGCCACTGGTGTTCAGCTG
                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                              Fujlyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes DNA, clone: AG088117
AG088117.1 GI:16639919
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                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes
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Sequencing: -21M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-086P15.F.
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                                                            tracking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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/lab_host="DH10B"
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Pred. No. 1.1e-10;
0; Mismatches 76;
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PTB-086P15.F, genomic survey sequence.
                                                                                                                                                                                                                                                                      Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                            Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White,Y., Wylie,T., Waterstow
WashU-NCI human EST Project
Unpublished (197)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA777621 538 bp mRNA linear EST 05-FEB-
zi95a07.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive
                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra, J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Thei White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      element ;, mRNA sequence. AA777621
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 515.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/111 c 163 g 149 t
                                                                                                                                                   /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1352757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                              /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
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Pred. No. 1.4e-06;
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-BT0254-220
300-019-c05&t3=2000-03-22&t4=1)
Seq primer: puc 18 forward
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A,{\bf J}\,. Shorgun sequencing of the human transcriptome with ORF expressed
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
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                                                                         note="Organ: breast; Vector: pucl8; Site_1: SmaI, Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Eco RI sites of the modified pT7T3 vector. Likwent through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

148 c 81 g 175 t
                                                                                                                                                                                                                                                                                                                                  ity sequence stop: 440.
Location/Qualifiers
                                                                                                                                                                                                                                       /dev_stage="Adult"
                                                                                                                                                                                                                                                          /clone_lib="BT0254"
                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                               'organism="Homo sapiens"
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Matches 73
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GSS.
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BE079777.1 GI:8470060
EST.
                                                                                                                                                                                                                                                                          73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 823 row: G column: 1:
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University of Washington
Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Construction of a Characterized Clone Resource for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B36584 475 bp DNA linear GSS 17-OCT HS-1041-A1-D06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=11 Row=G, DNA sequence. B36584
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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(206) 685-7301
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Hood,L.E.
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1 (bases 1 to 563)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-BT0627-140
200-011-A05&t3=2000-02-14&t4=1)
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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High quality sequence stop: 537
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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a 135 c 100 g 137 t 2 others
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1 (bases 1 to 678)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-BT0627-220
300-012-H08&t3=2000-03-22&t4=1)
Seq.primer: puc 18 forward
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High quality sequence stop: 563.
Location/Qualifiers
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Laboratory of Cancer Genetics
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                                                                                                                       M.J., Soares, F., Brentani, R.R.,
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144 c 100 g 144 t 1 others
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/clone_lib="BT0627"
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   Acad. Sci. U.S.A. 97
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(7), 3491-3496 (2000)
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Best Local S
Matches 73
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                                                                                    Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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AV731140 HTF Homo sapiens
AV731140 AV731140 GI:10840561
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Brazil
                                                                                                                                                                                                                                              Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zen,
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                ,S., Gu,W., Tu,Y., Jia,J., Fu,G., Chen,J., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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200-015-a03&t3=2000-02-12&t4=1)
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Location/Qualifiers
                                                      l: hanzg@chgc.sh.cn
clone is available at CHGC in
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                                  Location/Qualifiers
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/clone_lib="ST0197"
   /organism="Homo sapiens"
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3., Hu,R.,
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Query Match
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493 GAACCTTGAGCTTGAGAGAGAGATCATTTAGGGTATCTGGCAGAAGAAATTTCTAAGCAGCA 552
                       300 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAAGTTTCTAAGCAGCA 359
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Department of Biochemistry
Institute of Basic Medical Science, Peking Union Medical College
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Tel: 86-010-65296951
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone_lib="human bone marrow cDNA library"
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/dev_stage="Adult"
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/clone="HTFARB01"
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Pred. No. 2e-05;
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AAGCATTCAAGAGGTAACTTGGGTGCTGTTAAAGGCA

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BF881529
QV1-ET0181-031200-546-f03
BF881529
BF881529.1 GI:12271655
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 345)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                           Homo sapiens
                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are availabe from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
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CIT-HSP-2298M4.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="2298M4"
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/db_xref="GDB:7153856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBeloBAC11; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
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Pred. No.
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3 ET0181
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Query Match
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                           Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2-QV1-ET0181-031200-546-f03&t3-2000-12-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 89.
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                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:960"
/clone_lib="ET0181"
/dev_stage="Adult"
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96 c 57 g 106 t
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100.0%;
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Pred. No.
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1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                           Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib:PTB Chimpanzee Male
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Clone tracking errors.

PRIMERS

Sequencing: M13Rev
LIBRARY
Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.
Location/Qualifiers
Location/Qualifiers
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="pTB-094J73.R"
/sex="male"
/sex="male"
/cell_type="lymphoblast"
/sex="male"
/sex="male
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Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                            Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                       114.8
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91.6
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73.2
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_EUBCOMB.seq:*
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US-09-997-610-5
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US-09-997-610-7
 US-09-864-761-7075
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US-09-864-761-8938
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Compugen Ltd
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Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 15057, A
Sequence 2137, Ap
Sequence 220, App
Sequence 270, App
Sequence 3715, Ap
Sequence 3, Appli
Sequence 7075, Ap
Sequence 8643, Ap
Sequence 8938, Ap
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Sequence 6, Appli Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli	i ro	Sequence 7441, Ap Sequence 3, Appli Sequence 2556, Ap	Sequence 7399, Ap Sequence 8449, Ap Sequence 16494, A	Sequence 9802, Ap Sequence 8495, Ap Sequence 33019, A		24780, 83, Ar 8787,	Sequence 7, Appli Sequence 7, Appli Sequence 8932, Ap

## ALIGNMENTS

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; LOCATION: (2)...(1381)
US-09-997-610-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo s
FEATURE:
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APPLICANT: HOlloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/997,610 CURRENT FILING DATE: 2001-11-29 PRIOR APPLICATION NUMBER: US 60/253,924 PRIOR FILING DATE: 2000-11-29
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                                    AGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCAAGCCCCATCATC
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US-09-997-610-5
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Best Local S
Matches 396
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LENGTH: 1731
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APPLICANT: HOLLOWAY, James L.
APPLICANT: HOLLOWAY, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
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AGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA
                                           AATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAA
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; Sequence 7, Application US//
; Patent No. US20020156244A1
; GENERAL INFORMATION:
; APPLICANT: FOX, Brian
APPLICANT: HOLloway, Jame;
; TITLE OF INVENTION: ADIPOC
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US-09-997-610-7
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; LOCATION: (1)...(1377)
; OTHER INFORMATION: n = A,T,C
US-09-997-610-3
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US-09-997-610-3
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Best Local Similarity 60.5%;
Matches 239; Conservative 8
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LENGTH: 1377
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FILE REFERENCE: 00-96
CURRENT PROFESSORIES
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NAME/KEY: variation
LOCATION: (1)...(1377)
OTHER INFORMATION: Each n is independently A, T, G, or C.
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TYPE: DNA
ORGANISM: Artificial Sequence
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 INVENTION: ADIPOCYTE
                                                                                           US/09997610
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; Pred. No. 2.3e-80;
87; Mismatches 69
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: Sequence 15057, Application US/09960352

: Patent No. US20020137139A1
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                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GE
   SEQ ID NO 15057
LENGTH: 425
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7
LENGTH: 1731
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 239;
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)...(1731)
OTHER INFORMATION: n = A,T,C or G
:-09-997-610-7
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGGTGCATCATTGCAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCACAGGGGTCCTGTACAATGCCCCAGAGGGGATTTAAAGGAGGCCATGGGAGTCTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGYMGNGTNCCNGGNAAYTAYAYWSNWSNTTYGAYGTNGARYTNCAYCAYTGYAARGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZACRP13
      ID: 64-LIB34-036-Q1-E1-H8
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RESULT 7
US-09-960-352-220
; Sequence 220, A
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; LENGTH: 415
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB34-018-Q1-E1-B12
US-09-960-352-9137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9137
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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403
                                                                                                                                       283
                                                                                                                                                         119 AAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTTCCTTTCAAGCCCATCA 178
                                                                                                                                                                                                                                                                            163 CGGGGCCACCAGGACACCCAGGGCCTCCAGGTATAAGAGGGCCTCCAGGTATAAGAGGAA
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                                                                                                                                                                                                         223 TACCAGGTTTGCCAGGTCCGCCGGGAACTCCAGGACCAAGTGTAAAATGCCCATGCCACA
                                                                                                                                                                                                                               62 TACCACAATATACAGGA----GAAATAAGTGAAATGACAAAATGCCCCTGTCCTGATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GTCCGCCTTCACTGTGAAGCTCAGTGGCCAATTGCCGTCCCCTTCAAAGCCTGTGCCCTT 104
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nes 149; Conserv
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                            2 CTGGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT
                                                                                                                                       GACAGTCCGCCTTCACTGTGAAGCTCAGTGGCCAGTTGCCTTCCCCCTTCAAAGCCTGTGC
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CATGCAAGGTGGC
                                                                  CCTTCACAGAGGTCCTGTACAATGCCCAGAGAGACTTACAGGAGGACACTGGGGTCTTCA 402
                                                                                                    TCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTG
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                                                                                                                                                                                                                                                                                                                                                160;
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                              Score 93; DB 10;
Pred. No. 1.7e-19;
0; Mismatches 90
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Pred. No. 2.
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. 2.5e-26;
57;
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                                                                                                                                                                                                                                                                                                                                                                               Length 415
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Application US/09960352

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; NAME/KEY: unsure
; LCCATION: (277), (335)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 01-LIB34-084-Q1-E1-A9
US-09-960-352-220
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US-09-960-352-1786
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SEQ ID NO 220
LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
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Patent No. US20020137139A1
                                                                                                                                                                       Matches
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ
SEQ ID NO 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local :
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APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                                                                                                                                                                                                                                                                                            LENGTH: 392
TYPE: DNA
ORGANISM: Bos taurus
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213 TACCAGGTTTGCCAGGTCCGCCGGGAACTCCAGGACCAAGTGTAAAATGCCCATGCCACA
                                                                               153 CGGGGCCACCAGGACACCCAGGGCCTCCAGGTATAAGAGGGCCTCCAGGTATAAGAGGAA
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                                       62 TACCACAATATACAGGA---GAAATAAGTGAAATGACAAAATGCCCCTGTCCTGATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 23.1%;
Local Similarity 76.7%;
                                                                                                            2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT
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                                                                                                                                                                 Score 82.2; DB 10;
Pred. No. 3.9e-16;
0; Mismatches 88;
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Pred. No. 4.4e-19;
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SEQ ID NO 3715
LENGTH: 410
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Best Local
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                                                                               AGCTAGGGCTCATGAAGAATGACACT
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Sequence 11516, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:

APPLICANT: Warren, Wester APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C.

Wesley C.

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; OTHER INFORMATION: Clone ID: 16-LIB34-024-Q1-E1-D7
US-09-960-352-3684
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SEQ ID NO 11516
LENGTH: 374
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                                                                                                                                                                                                                           Matches 120;
                                                                                                                                                                                                                                               Query Match
Best Local
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15112
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 49-LIB34-046-Q1-E1-E2
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                                                                                             CACAGGGGTCCTGTACAATGCCCAGAGGGATTTTAAAGGAGGCCATGGGAGTCTTTGCTTG
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                                                                                                                                                  GTCTGCCTTTTCCGTCAAGCTGAGTGGGCCTTTCCCAGGACCCTCCCAGCCCCATTGTCTT 219
                                                                                                                                                                                       GTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTTCCAAGCCCATCATCTT 182
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CAGCGTCCCTGGTGTACCACTTTGGCTTTGACATTGAGTTGTTTCAGAGTGCTGTCAA
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Pred. No.
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Pred. No. 2
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2.8e-13;
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; NAME/KEY: unsure
; LOCATION: (377)
; OTHER INFORMATION: unsure at
; OTHER INFORMATION: Clone ID:
US-09-960-352-4241
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                                                                                                                                                                                                                                                                            Sequence 25080, Application US/09864761 Patent No. US20020048763A1
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SEQ ID NO 4241
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APPLICANT: Penn, Sharron G.
APPLICANT: Hansk, David R.
APPLICANT: Hansel, David K.
APPLICANT: Hansel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLE
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(1029))C
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CURRENT FILING DATE: 2001-09-24
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                              451
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2000-05-26 WUMBER: US

09/632,366

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RESULT 14
US-09-864-761-8349
; Sequence 8349, Application US
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
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; OTHER INFORMATION:
US-09-864-761-25080
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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PILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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SSED IN HELA, SIGNAL = 6.1
SSED IN ADULT LIVER, SIGNAL = 2.8
SSED IN BONE MARROW, SIGNAL = 1.8
SSED IN HEART, SIGNAL = 5.5
SSED IN PLACENTA, SIGNAL = 2.5
SSED IN PLACENTA, SIGNAL = 7.00e-78
T: AL163210.2, EVALUE 6.80e-71
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TITLE OF IN
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TYPE: DN
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ORGANISM: Homo
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 314
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
               GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA
                                                         GGGGAACATTGAACTTGAGAGAGAGATGATTTGGGGTATCTGGTGGAAGAAATTTCTAAACA 313
                                                                        GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA
                                                                                                                                   Similarity
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NUMBER: PCT/US01/00663
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                                                                                                                                                                                          MAP TO AL121767.3
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Pred. No. 1.3e
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FEATURE:

OTHER INFORMATION: MAP TO AC006337.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 14

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 13
                                                                                                               US-09-864-761-2925
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US-09-864-761-2925
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Query Match
Best Local Similarity 74.3
Matches 72; Conservative
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 2925
LENGTH: 1946
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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TYPE: DNA
ORGANISM: Homo sapiens
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OR APPLICATION NUMBER: PCT/US01/00665
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OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00663
OR APPLICATION NUMBER: PCT/US01/00663
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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y Match Local Simil hes 158; (	ULIT 1  08 - 463-911-6  equence 6, Applicat  atent No. 5869330  GENERAL INFORMATION  APPLICANT: Schery  APPLICANT: Lodisi  TITLE OF INVENTION  TITLE OF INVENTION  INUMBER OF SEQUENCY  CORRESPONDENCE ADD  ADDRESSEE: Ham  STREET: Two Mi.  CITY: Lexingto  STATE: Massach  COUNTRY: USA  ZIP: 02173  COMPUTER READABLE  MEDIUM TYPE: F.  COMPUTER READABLE  MEDIUM TYPE: F.  COMPUTER IBM I  OPERATING SYSTE  SOFTWARE: Patel  CURRENT APPLICATION NUM  FILING DATE:  CARSIFICATION NUM  FILING DATE:  CARSIFICATION NUM  TELEPAN: (617)  TELECOMMUNICATION  TELEPANE: (1313)  TYPE: TOPOLOGY: Lines  MOLECULE TYPE: DI  FEATURE: CDS  MOLECULE TYPE: DI  FEATURE: CDS  LOCATION: 731  08-463-911-6	330000000000000000000000000000000000000
ilarity Conservat	ILT 1  B-463-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  94-63-911-6  PPLICANT: Scherer, Philipp E APPLICANT: Scherer, Philipp E APPLICANT: Codish, Harvey F.  APPLICANT: Lodish, Harvey F.  APPLICANT: Codish, Harvey F.  APPLICANT: Lodish, Harvey F.  TITLE OF INVENTION: A NOVEL S  TITLE OF INVENTION: EXCLUSIVE  NADRESSEE: Hamilton, Brook, STREET: Two Militia Drive  CITY: Lexington  STATE: Massachusetts  COUNTRY: USA  ZIP: 02173  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC Compatible  OPERATING SYSTEM: PC-DOS/MS  SOTWARE: Patentin Release  CURRENT APPLICATION NUMBER: US/08/4  FILING DATE:  APPLICATION NUMBER: WHOME COMPUTER ARE STRATION: 100: 6:  SEQUENCE CHARACTERISTICS: LENGTH: 131 base pairs  TYPE: Nucleic acid  STRANDEDNESS: single  TOPOLOGY: Linear  MOLECULE TYPE: DNA (genomic)  FEATURE:  MALE/KEY: CDS  LOCATION: 73804  18-643-911-6	
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APPLICANT: Sheppard,
Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
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Best Local Similarity 48.9
Matches 158; Conservative
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EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEO ID NOS: 47
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                                  303 TATTTGGCTAATGAGGAAGCAAA 325
                                                                                                         243 CAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGAA 302
                                                                                                                                                                                183 CACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTGCTTG
                                                                                                                                                                                                                                                                                              308 TCCGGGAATCCAAGGCAGGAAAGGAGAACCTGGAGAAGGTGCCT-----ATGTATACCG
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                                                                                                                                                                                                                                                                                                                                                                                                       3 TGGACCTCCAGCACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTT 62
                                                                                                                                                                                                                                                                                                                     ACCACAATATACAGGAGAAATAAGTGAAAATGACAAAATGCCCCTGTCCTGATATAGAAAG
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                                                                                                                                                TACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTG
                                                                                                                                                                                                                       CTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTT
                                                                                                                                                                                                                                                         GTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCAAGCCCCATCATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTGCTTG
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48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.6; DB 4;
Pred. No. 3.3e-05;
0; Mismatches 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-217
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated Fr
TITLE OF INVENTION: and Methods For Their Us
FILE REFERENCE: 11000.1011c1
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                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5869330
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Best Local Similarity
Matches 103; Conserv
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LENGTH: 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 348
                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
              ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Scherer, Philip
APPLICANT: Lodish, Harvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734
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                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                STREET: Two Mil.
CITY: Lexington
STATE: Massachu
                                 CLASSIFICATION:
                                                                                                                                                                                               COUNTRY: U
ZIP: 02173
                                                  FILING DATE:
                                                                   APPLICATION NUMBER: US/08/463,911
                                                                                                                                                         MEDIUM TYPE:
NAME
                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                      Two Militia Drive
                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                     Hamilton,
             INFORMATION
                                                                                                                                                         Floppy disk
                                   530
                                                                                                                                                                                                                                                                                                                                       Philipp E.
Harvey F.
A NOVEL SERUM PROTEIN PRODUCED
EXCLUSIVELY IN ADIPOCYTES
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Pred. No. 0.00038;
0; Mismatches 101
                                                                                                                                                                                                                                                                                     Smith & Reynolds,
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CURRENT APPLICATION NUMBER: US/09/336,536; CURRENT FILING DATE: 1999-06-18; NUMBER OF SEQ ID NOS: 75; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 2; ELENGTH: 728; TYPE: DNA; ORGANISM: Homo sapiens
US-09-336-536-2
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Best Local Similarity
                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Applic
Patent No. 6406884
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                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Leiby, K.
APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9940
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
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                                                                     405
                                                                                                                                                                   154 CTTCCTCTTCCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 CTTATATGTATCGCTCAGCGTTCAGTGTGGGGGCTGGAGACCCGGGTCACTGTTCCCAATG 436
465 CATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGG
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                              274 GATGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 TGAAAGATGTGAAGGTGAGCCTCTTCAAGAAGGACA 592
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                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                 TTAAAGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTT 273
                                                                 TACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTC
                                                                                                                                    CCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACA 556
                                                                                                                                                                                                               96;
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09336536
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46..786
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                                                                                                                                                                                                                          Score 37.4; DB Pred. No. 0.013;
                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                          DB 4;
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                                                                   464
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; LOCATION: (198)...(926)
US-09-140-804-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-1
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US-09-140-804-1
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Patent No. 6406884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09140804 Patent No. 6197930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO
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Best Local Similarity 51.5%;
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APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/140,804 CURRENT FILING DATE: 1998-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O. APPLICANT: Humes, Jacqueline M.
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/056,983 EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1347
214 TTAAAGGAGGCCATGGGAAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTT 273
                                                                543 CCTCCGCCGTCTGACGCACCCTTGCCCCTTCGACCGCGTGCTGGAACGAGCAGGGACAT
                                                                                                     154 CTTCCTCTTCCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGAT 213
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Similarity 51.5%;
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Pred. No. 0.018;
0; Mismatches 81;
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                                                                                                                                                                 Score 37.4; DB Pred. No. 0.018;
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US-08-687-080-59
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                                                                                                                                                                      Patent No. 5965427 GENERAL INFORMATION:
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Patent No. 6197930
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LENGTH: 729
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O. APPLICANT: Humes, Jacqueline M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Degenerate nucleotide sequence encoding OTHER INFORMATION: polypeptide of SEQ ID NO:2.
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STREET: 550
CITY: Palo Alto
                                                                                                                                  APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human R
                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                        ADDRESSEE:
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86; Conserv
                                                  E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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                                                                                                                                  Human RAD50 Gene and Methods of Use Thereof
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Pred. No. 0.032;
3; Mismatches 189;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09146053A Patent No. 6399349
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Best Local
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                                                                                                                                                                                                                                                                                                               APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/057,854 EARLIER FILING DATE: 1997-09-02 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/146,053A CURRENT FILING DATE: 1998-09-02
                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                    FILE REFERENCE: MCG103
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Human Aminopeptidase P Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
 38040
                                                                                                                                                                 LENGTH:
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FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIF TO LATER PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/592,126
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            339 GGAAGAATTTCTAAGCAGCAAAGCATTCAAGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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GGAAGAATTTCTAAGCAGCAAAACATTCAAGAGGT
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41; Conservative
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                                                           Conservative
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                                                                       Score 34.4;
Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09422869 Patent No. 6235481 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                 Matches
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09415551 Patent No. 6369295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 57114-A
CURRENT APPLICATION NUMBER: US/09/415,551
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cheah, Kathryn
APPLICANT: Cheung, Kenneth
TITLE OF INVENTION: USES OF TRANSGENIC ANIMALS
TITLE OF INVENTION: MUTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ODA, NAOHISA
APPLICANT: SREEMAN, SEAMUS
APPLICANT: SREEMAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: POLONSKY, APPLICANT: HORIKAWA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/134,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                             LENGTH: 459
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                  230
                                                                                                                                 110 CTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCA 169
                                                                                                                  83
GAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCA 287
                                               CCCCCATCCCATTTGATGAGATTCTGTACAATAGGCAGCAGCATTACGACCCAAGATCTG
                                                                              AGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGG
                                                                                                             CAGGTATGCCCGTGTCTGCTTTTACTGTCATTCTCTCTAAAAGCTTACCCCAGCAGTAGGTG 142
                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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ilarity 49.4%;
Conservative
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78.8%;
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                                                                                                                                                                                             Score 34; DB 4
Pred. No. 0.13;
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Pred. No. 1
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                                                                                                                                                                                                            DB 4; Length 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                              90;
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641 CTCCAGGACCTCCTGGTGCTATAGGT

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PATENT NO. 617182/
PATENT NO. 617182/
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILLING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
δÃ
                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE; OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS US-09-029-348-20
                                     망
                                                                       Qy
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US-09-415-551-1
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No. 6171827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09415551 Patent No. 6369295 GENERAL INFORMATION:
                                                                                                                Matches
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                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 486
TYPE: DNA
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cheah, Kathryn
APPLICANT: Cheung, Kenneth
TITLE OF INVENTION: USES OF TRANSGENIC ANIMALS CONTAINING A TYPE X COLLAGEN
TITLE OF INVENTION: MUTANT
FILE REFERENCE: 57114-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/415,551
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                    LENGTH: 1881
TYPE: DNA
                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 CTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 CCCCCATCCCATTTGATGAGATTCTGTACAATAGGCAGCAGCATTACGACCCAAGATCTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAAGGAGGCCATGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
62 TACCACAATATACAGGAGAAATAAGT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 CAGGTATGCCCGTGTCTGCTTTTACTGTCATTCTCTCTAAAGCTTACCCAGCAGTAGGTG 142
                                                                                                                                    Local
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                                                                          2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 61
                                       CTGGATCTCCAGGATACCAAGGACCCCCTGGTGAACCTGGGCAAGCTGGTCCTTCAGGCC 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATCTTTACCTGTAAGATCCCAGGCATATACTATTTCTCCTACCACGTGCATGTGAA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATCTTTACCTGTAAGATCCCAGGCATATACTATTTCTCCTACCACGTGCATGTGAA 260
                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Conserv
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09029348
                                                                                                                Conservative
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                                                                                                                                8.4%;
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                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                Score 33.2; DB Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 4
Pred. No. 0.14;
                                                                                                              Mismatches
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                                                                                                                                                DB 4;
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3.
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RESULT 15
US-09-426-290-1/c
Sequence 1, Application US/09426290
Fatent No. 6410712
GENERAL INFORMATION:
APPLICANT: Jeffrey Gulcher
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT FILLING DATE: 199-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE STATE 109-10-25
NAME/KEY CDS
LCCATION: (21181)...(21403)
AME/KEY CDS
LOCATION: (210753)...(101996)
NAME/KEY CDS
LOCATION: (101054)...(110439)
NAME/KEY CDS
LOCATION: (110324)...(110439)
NAME/KEY CDS
LOCATION: (12058)...(124278)
NAME/KEY CDS
LOCATION: (120709)...(127130)
NAME/KEY CDS
LOCATION: (120810)...(129139)
US-09-426-290-1

QUETY MATCH
Best LOCAL Similarity 75-9%; Pred: No. 4-9;
MATCHES 41; Conservative 0; Mismatches 13; Indels 0; G
Oy 336 TAAGGAAGAAATTTTTAAGGACCAAAGCATTCAAGAGGTGACTTGGCTACTTTT 54031
Job time: 231.142 secs
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Gaps

0;

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Result
No.
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on:
                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                         Score
    351
58.6
58.4
58.4
58.4
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58.4
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                                                                                                                                                      Query
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                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 1.0
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396
    88.6
14.8
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11:
13:
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                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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Listing first 45 summaries
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                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
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                                         AAL44066
AAC24351
ABA75076
ABA39760
AAK23591
AAK49719
               AAI26826
AAI55610
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                                                                                                                                       Description
               Human
Probe
Probe
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Probe
Human
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            n genset metab
n secreted pro
n foetal liver
e #18226 for g
brain expres
n bone marrow
e #16759 for g
e #24296 used
  for g
RESULT 1
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                            18-JUL-2002.
                                                      WO200255694-A2
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                                                                                                                                                                                                                                                                                                                                                                              AAL44066;
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                                                                                                                                                                                Homo sapiens.
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14.0	14.0		14.0			•			14.1	14.1	14.1	14.1	•	٠	14.2		14.4	14.4		14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4				14.7		
070	520	520	520	520	520	342	1054	505	505	505	505	505	505	72215	32127	32127	1946	1946	1946	1946	1946	1946	1946	1946	1946	1077	999	930	686	662	519	519	519	519	519	
22	22	22	22	22	22	21	23	24	22	22	22	22	22	22	22	22	24	22	22	22	22	22	22	22	22	23	23	23	22	22	22	22	22	22	22	
AA142928	1794	$\vdash$	AAK11311	ABA30177	ABA62906	AAC26950	AAS64468	ABS09176	AAI40252	AAK34535	AAK08648	ABA28609	ABA60370	AAK86832	AAI63605	AAI99255	ABS02918	AAI02893	AAI34334	AAI12975	AAK28410	AAK02964	445	67	ABA44227	265	083	AAS81134	2391	1506	54	762	676	109		
Probe #11014 used	robe #7875 f	Human bone marrow	expr	Probe #8643 for ge	foeta	Human secreted pro	DNA encoding novel	Human genome-deriv	Probe #8938 used t	=	brain expi			immune/haem	Human kidney relat	Human excretory re	Human genome-deriv	Probe #2884 used t	Probe #3020 used t		=	brain expi	#2925 f	foetal		encoding	DNA encoding novel	9	breast canc	breast	#11227 use	#7554	bone m	brain expre	Probe #8349 for ge	

## ALIGNMENTS

ВP

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AC AAL44066;

XX

XX

Z7-SEP-2002 (first entry)

XX

XX

Human genset metabolic gene (GMG-9) cDNA sequence.

XX

Human; gene; ss; gene therapy; genset metabolic gene; GMG-7B; GMG-7B; GMG-8; GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity; GMG-8; GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity; KW impaired glucose tolerance; insulin resistance; Syndrome X;

XX

Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; KW heart diabetes; hyperlipidaemia; atherosclerosis; hypertension; KW high blood pressure; insulin sensitiser;

XX

XX

Non-insulin dependent diabetes mellitus.

XX

XX

YX

Homo sapiens.

Location/Qualifiers

FT

/*tag= a
/partial
/product= "Human GMG-9 protein"
/note= "No stop codon is given"

XX

XX

XX

W0200255694-A2.
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RESULT 2
AAC24351
ID AAC24351
XX
AC AAC2
XX
XX
DT 06-C
DT 06-C
XX
XX
C
DT UMBER
C
DT UMB
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Best Local S
Matches 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present cDNA sequence encodes the human GMG-9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-9, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                         gene
                                                                                                     Human;
                                                                                                                                                                       Human secreted
                                                                                                                                                                                                                                            06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obesity,
      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          AAC24351 standard; cDNA; 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1338 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2001; 2001US-262235P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 TGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGAGCTGCATCATTGCAAGGTGAATATTTTGGCTAATGAGGAAGCAAATTTTTGGCTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTTCCTTTCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAATGTCCTGGTGCCCCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA
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                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC
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                                                                                                     EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 122-124; 128pp; English.
                                                                                                                                                                                                                                         (first entry
                                                                         chromosome
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                                                                                              expressed
                                                                                                                                                                       protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
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                                                                  sequence
mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 C; 350 G; 341 T; 0 other;
                                                                                                                                                                       EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 351; DB 24;
Pred. No. 2.3e-104;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                       SEQ ID
                                                                     tag; secreted protein; cDNA isolation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanaka
                                                                                                                                                                       NO: 28426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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   ID XXX AC XXX AC
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04-FEB-2000;
26-MAY-2000;
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RESULT 3
ABA75076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                Human;
                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #23381
                                                                                                                                                                                                   01-FEB-2002
30-JAN-2001; 2001WO-US00669
                                    09-AUG-2001
                                                                 WO200157277-A2
                                                                                                                                                                                                                                  ABA75076;
                                                                                                                                                                                                                                                                 ABA75076 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                 207
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                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                   AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                          GAACTTTGAACTTGAGAGAAATGATTTAGGATATGTGGTGGAAGAAATTTCTAAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                   AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA
                                                                                                                                  foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID 28426; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  torensic,
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                                                                                                                                                                                                 (first entry)
                                                                                                                                  liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ů,
                                                                                                                                  gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%;
75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 55 C; 101 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 58.6; D; Pred. No. 8e-0 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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2000US-0180312 2000US-0207456

The

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RESULT 4
ABA39760
ID ABA3
XX ABA3
AC ABA3
AC ABA3
XX Huma
KW Card
KW Card
KW Card
KW Cong
XX Homc
XX Homc
XX Homc
XX Homc
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                               03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; heart; microarray; vascular syste cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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2000US-0608408
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2000US-0234687
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2000US-0024263
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Pred. No. 7.6e-09
0; Mismatches 2
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
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04-OCT-2000;
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Note: The sequence data for this patent did not specification, but was obtained in electronic for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 273
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s disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes
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Pred. No. 7.
                                                      Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĮĎ
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format
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RESULT 6
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27-SEP-2000;
                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single
brains
probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                  microarray;
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                            The present invention
                                                  Example
                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                             WO200157276-A2
                                                                                                                                                                                                                                                                                                                             Human;
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                                                                                                                     Penn
                                                                                                                                       (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                bone
                                                                             genome-derived
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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                             provides a number of single exon nucleic
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                                                 24276; 658pp +
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                                                                                                                                                                                                                                                                                                                           exon; gene expression
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Pred. No. 7
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                                                                                                                    Rank
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                                                Sequence Listing;
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les 26;
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                                                                            probes useful
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RESULT 7
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Best Local
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                                                                                                         (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WII specification, but was obtained in electronic format directly from WII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such
the f
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03-AUG-2000;
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                 Match
                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n as lymphoma,
probes of the
                                                                                                                                                                                                                                                                  present invention relates to human single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SG,
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                          ID No 16759;
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Score
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Pred.
                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression;
                                                       G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.4;
No. 7
58.
                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
                                                                                                                                                                                                                                                                                                                                                                                                                                             DR
8.4;
5. 7
                                                         ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
 DB 22;
.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelial cell;
                                                                                                                 part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273;
                                                                                                                                                                                                                                                                                                                                                      s for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                    probes
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                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Similarity

DNA; 519 BP.

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ABA62555 standard;
                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                    Homo sapiens
                                             01-FEB-2002
                                                                                                                                                                                   26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-2002
                                                                                                                                      09-AUG-2001
                           ABA62555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA29883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA29883
 ABA62555
           qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                          to measure gene expression in human placenta sample.
                  GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GGGGAACATTGAGAGAGAGATTTGGGTATCTGGTAGAAATTTCTAAACA 174
                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
                                                      GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.4; DB 22;
Pred. No. 7.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing gene expression in human placenta
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID No 24296; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
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                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                        2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.78;
74.08;
                                                                                                                   AAI55610 standard; DNA; 273
                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                    2000GB-0024263
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 74.0 tes 74; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                     genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53
                                                                                                                                                                         Probe #24296 used
                                                                                                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                                                                                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                21-SEP-2000;
27-SEP-2000;
                                                                                                                                                       17-OCT-2001
                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                       26-MAY-2000;
74;
                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                            Probe;
                                   115
                                                                      175
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                  297
                                                     357
                                                                                                                                                                                                                       Homo
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Matches
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 GCTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #8349 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 10860; 639pp + sequence listing; English.
                                                Human foetal liver single exon nucleic acid probe #10860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 58.4; DB 22;
74.0%; Pred. No. 1.1e-08;
tive 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-053366.
; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483447/52
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                                                                                                                                                                                                                    40200157277-A2
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RESULT 9

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Homo sapiens
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                                                                                                                                                                                                                                                    orains
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK36769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
Human; gene expression; heart; microarray; vascular system; probe;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Match 14.7%; Score 58.4; DB 22; Length 519; Local Similarity 74.0%; Pred. No. 1.1e-08; nes 74; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe SEQ ID NO: 10902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 8349; 530pp; English.
                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                      Chen W,
                                                                                                                           2000us-0180312.
2000us-0207456.
2000us-0608408.
2000us-063236.
2000us-0234687.
                    congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK10911 standard; DNA; 519
                                                                                                       30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                         WPI; 2001-488899/53
                                                             40200157274-A2
                                                                                                                                                           03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                          Homo sapiens
                                                                                                                                      26-MAY-2000;
                                                                                                                                                                                           04-OCT-2000;
                                                                                                                            04-FEB-2000;
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                                                                                   09-AUG-2001
                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK10911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 10902; 650pp + Sequence Listing; English.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed single exon probe SEQ ID NO: 11326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 58.4; DB 22; Length 519; 74.0%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
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0
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                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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26-MAY-2000; 2000US-0207456.
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                                                                                             30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483446/52
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WO200157275-A2.
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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Local Sim.
74;
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                                               09-AUG-2001
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(SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for mesauring human gene expression in a sample derived from human cervical epithelial cells. By mesauring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP).
                                                                                           human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #11227 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                              297 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                   Score 58.4; DB 22; Length 519;
Pred. No. 1.1e-08;
0; Mismatches 26; Indels 0;
                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                         Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 353
                                                                                                                                                                                                                                                                                                                                                                                                       357 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human placenta
                                                            Claim 25; SEQ ID No 7554; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID No 11227; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                            present invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                    / Match 14.7%;
Local Similarity 74.0%;
nes 74; Conservative
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2000US-0207456.
2000US-0608408.
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #7554 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                             297 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 GGGGAACATTGAACTTGAGAGAGATGATTTGGGGTATCTGGTGGAAGAAATTTCTAAACA 313
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                      Example 4; SEQ ID NO: 11326; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                       Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    / Match 14.7%; Score 58.4; DB 22;
Local Similarity 74.0%; Pred. No. 1.1e-08;
Nes 74; Conservative 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                              analyzing gene expression in human bone marrow
                                                                                                                      Rank DR;
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                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                              the probes of the invention.
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2000US-0234687.
2000US-0236359.
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                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer; ss
                                                                                                                                                  WPI; 2001-488900/53
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                                            27-SEP-2000;
04-OCT-2000;
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                              21-SEP-2000;
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 30-JUN-2000;
                03-AUG-2000;
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The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to human breast cancer expressed polynucleotides
                                                                                                                                                                                                    297 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 356
                                                                                                                                                      Gaps
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                                                                                                                ch 14.7%; Score 58.4; DB 22; Length 519; Similarity 74.0%; Pred. No. 1.1e-08; 74; Conservative 0; Mismatches 26; Indels 0
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Pred. No. 3.5e-08;
0; Mismatches 40; Indels
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                                                                                 Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cancer expressed polynucleotide 7520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                       GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                                                       BP
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14-MAR-2000; 2000US-0189167.
24-MAR-2000; 2000US-0193099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-02052330.
09-UUN-2000; 2000US-021315.
25-JUL-2000; 2000US-021315.
                                                                                                                                                                                                                                                                                                                                                                     AAL15063 standard; cDNA; 662
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Similarity 66.9%;
81; Conservative
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TGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAA 335
                                          331 TITITCCCCTGCCCTAGAGAITTGTGGAACTTTGAACTTGGAGGATGATTTAGGGTATCT 390
                                                                                     TAAGGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAAGGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 145880)
Bridgeman A.
Direct Submission
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Homo sapiens
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

Human DNA sequence from clone RPI-302D9 on chromosome 22 Contains 6SSs, complete sequence.
282198
47G. AC104256 Homo sapi AC007433 Homo sapi AC027433 Homo sapi AC025112 Homo sapi AC01553 Homo sapi AL157884 Human DNA D12976 Tamlas asia D12975 Tamias asia AB069679 Callosciu 282198 Human DNA s ALO08722 Human DNA D12974 Tamias asia AB067779 Tamias si ramias asia Human PAC Homo sapi Z82198 Human DNA s Human DNA sapi sapi Human DNA Ното зар Homo sap Homo sap score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Homo R Ношо Ношо Ношо Ношо Homo Homo Homo AL441943 AC069566 AC092609 AC062031 AC02267 AC02867 AC018971 AC011418 AC011418 AC013303 ALIGNMENTS TMSHP25 AB067813S3 HS302D9 SUMMARIES TMSHP20A AB067779 HS732E4 AC104256 AL359258 AC023471 AC0224910 AC022379 AC008012 AC074266 AC019185 AC025112 AC015553 AL161623 AL157884 AC073840 HS302D9 ID DB Query Match Length 88.6 145880 36.9 1265 144514 149038 176932 79848 203234 69937 5881

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                 CB10 ISA, UK. E-mail enquiries: hunguery deanger, cank Clone requests: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm., EMBL; Sw., SWISSPROT: Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be form on the WORMPEP database can be forestal close contige of human chromosome 2.2, constructed by the Sanger Centre Chromosome 2.2 constructed by the Sanger Centre Chromosome 2.2 http://www.sanger.ac.uk/HGP/Chr22

RPI-302D9 is from the library RPI-1 constructed at the Roswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: pCYPAC2
This sequence is the entire insert of clone RP1-302D9 The true left
end of clone CTA-282F2 is at 69682 in this sequence. The true right
end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2350. .2660

Anote—"AluSc repeat: matches 3. .309 of consensus" 2684. .2981

Anote—"AluSq repeat: matches 2. .300 of consensus" 3323. .3343

Anote—"MarThe repeat: matches 116. .136 of consensus" 3344. .3652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .568 of consensus"
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/note="L2 repeat: matches 2579. .2705 of consensus"
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note="Alusx repeat: matches 1. .312 of consensus"
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/note="AluJb repeat: matches 1. .311 of consensus"
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/note="AluSp repeat: matches 1. .299 of consensus"
1450. .1583
/note="MIR repeat: matches 24. .160 of consensus"
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//note="MER3 repeat: matches 1. .144 of consensus"
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/note="MLT1E repeat: matches 5073. .5176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
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/clone_lib="RPCI-1"
188 .245
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/note="L2 rep
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/note="52 cor
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  JOURNAL
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                                                                         COMMENT
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/note="MLT1B repeat: matches 119. .178 of consensus"
15728. .16027
                                                                                                                                             7775. 8060
/note="AluJo repeat: matches 1. .295 of consensus" 8414. 8551
/note="L2 repeat: matches 2553. .2706 of consensus" 8914. 9030
/note="MIR_repeat: matches 147. .262 of consensus" /note="MIR_repeat: matches 147. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2275 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2239 of consensus"
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14597. .15201
/note="match: GSS: Em:AQ553482"
/14616. .15060
/note="match: GSS: Em:AQ370601"
/14868. .15040
/note="MIR repeat: matches 49. .233 of consensus"
/15071. .15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluY repeat: matches 1. .301 of consensus" 14368 .14452 /note="MIR repeat: matches 141. .225 of consensus" 14589 .14679
                                                                                       .77 of consensus"
                                                                                                                 7482. .7754
/note="AluJb repeat: matches 9. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 174. .244 of consensus"
13398. .13698
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                                            .302 of consensus"
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13806. .13919
/note="MIR repeat: matches 77. .189 of consensus"
13945. .14060
/note="MIR repeat: matches 24. .142 of consensus"
14061. .14367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="MLT1B repeat: matches 1. .99 of consensus"
                                                                                                                                                                                                                                                                                           .241.of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .150 of consensus"
                                                                                                                                                                                                                                                                                                                                       9283. .9412
/note="MIR repeat: matches 15. .144 of consensus"
9521. .9679
/note="FAM repeat: matches 3. .161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .137 of consensus"
.23 of
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10718. 11310
/note="match: GSS: Em:B14024"
/note="match: GSS: Em:B43656"
/note="match: GSS: Em:B43656"
/note="MIR repeat: matches 20. 13
12174. 12445
/note="L2 repeat: matches 1988. 2
/1244. 12642
/note="MIR repeat: matches 1988. 2
/1244. 12642
                                                                                                                                                                                                                                                                                                                                                                                                                                 9820. 10225

/note="MSTB repeat: matches 2. .4

complement(10179. .10678)

/note="match: GSS: Em:B56592"

/note="match: GSS: Em:AQ701486"
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15669. .15727
                                                                  /note="MADE1 repeat: matches 23. 7482. .7754
  matches 1.
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13699. .13810
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[5304. .15399
                                            matches 1.
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  MADE1 repeat:
                                          /note="AluSx repeat: 5988. .7036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(10249. . . /note="match: GSS: 10312. .10383
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13331. 13397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37314 AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC 37373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCTTCCTTTCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 TTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATA 337
                                                                                                                           of
                                       .390 of consensus"
                                                                                                                                                                                                 .4919 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
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                                                                                                                                                                                                                                                                                                                                                                                      /note="Alusgi repeat: matches 1. .306 of consensus"
21239. .21553
                                                                                                                                                                                                                                                                                                                                                                                                                                              //note="THEIB repeat: matches 1. .364 of consensus"
22302. .22537
/note="MER66-internal repeat: matches 2186. .2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .313 of consensus"
                                                                                                                                                                      of consensus"
            .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23905. .23989
/note="MER66-internal repeat: matches 3017. .3102
                                                                   .300 of consensus"
                                                                                             .29 of consensus"
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                                                18393. .18712
/note="AluJb repeat: matches 1. .311 of cons
18713. .19133
/note="MER66-internal repeat: matches 4548.
                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ005063"
19251. .19719
/note="match: GSS: Em:B14179"
19537. .20290
20317. .20382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER66-internal repeat: matches 1210.
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                                       178.
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ilarity 98.6%; Pred. No. 2.4e-94;
Conservative 0; Mismatches 5;
/note="AluSc repeat: matches 1.
16028. .16245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                             20317. .20382
/note="33 copies 2 mer ta 68 (20513. .20666
20513. .20666
20682. .21008
                               /note="MLT1B repeat: matches
16546. .16854
                                                                                                                                                                                                                            complement(18872. .19230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .22850
                                                                                                                                                                                                              consensus
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Matches 354; Conserv
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RESULT 2 TMSHP20A

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/trānslation="MTDVWRLAIFVLMVNVLNDQVSCSGPPGPVGYPGVPGPPGP

PGQPGAAGRECDPGRGPSVKCPCRRSAFTVKFSGRLPPPSEPVVFTEVLYNYQRDL

PGSTGVFNCVPPGNYHFSFPVELYHCKVKIGLMKNHIQVMEKHQLSKNEYENSGAMI

MPLRQGDXVWLEADVETEEPDQAKVVIYFSGFLISS"
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 ROD 03-FEB-1999
                                                                                                                                                                                                                                                                                                               Takamatsu, v. Direct Submission Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Labbratory of Molecular Biology; Par:0427-78-9408, Par:0427-78-9408,
                                                                                        protein.

Tamias aslaticus liver cDNA to mRNA, clone:pCM20-7.

Tamias sibiricus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Scluridae; Sclurinae;
                                                                                                                                                                                                                        and Shiba,T.
plasma proteins with a
                                                      D12974.1 GI:287467
HP-20; collagen-like domain; hibernation-related proteln; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCAAGCCCATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGA
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   linear
                                                                                                                                                                                     1 (bases 1 to 1265)
Takamatsu,N., Ohba,K., Kondo,J., Kondo,N. and Hibernation-associated gene regulation of plas collagen-like domain in mammalian hibernators Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
                   complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 146.2; DB Pred. No. 7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Tamias sibiricus"
/db_xref="taxon:64680"
/clone="pcM20-7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="collagen-like domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA02351.1"
/db_xref="GI:287468"
Tamias asiaticus mRNA for HP-20, D12974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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1238. .1243
1265
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/product="HP-20"
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MPLRQGDKVWLEADVETEEPDQAKVVIYFSGFLISS"
                                                                                            ROD 26-OCT-2001
                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                 Ono,M., Hosoe,Y., Azuma,S., Shoji,M., Nara,K., Kondo,N., Shiba,T. and Takamatsu,N.
HNF-1 regulates the liver-specific transcription of the chipmunk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-AUG-2001) Motoharu Ono, Kitasato University, Department of Biosciences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:ms)99805m@stu.sci.kitasato-u.ac.jp, Tel:81427789408, Fax:81427789408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 CCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATG 228
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complete cds.
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/gene="HP-20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonym:Tamias asiatious"
1518. 1684
join(1678. 1684,2573. .2710,3968
/gene="HP-20"
join(1678. .1684,2573. .2710,3968
                                                                                                                                                                        Tamias sibiricus DNA, clone:lamdaCM20G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Tamias sibiricus"
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/clone="lamdacM20G1"
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                                                                                     Tamias sibiricus gene for HP-20, AB067779
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Gene 277 (1-2), 121-127 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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| ||| || || || ||| ||| || || || || || AGATIGGGIIGAAGAACCACAI 504
                                                                                                                                         AB067779.1 GI:15706341
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3968 .5000
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PGPPGIPGFPGAPGALGPPGPPGPFGPGPPGPGDVEKCSSRPKSAFAVKLSERPPE
PROPIVFKEALYNDEGHFNMATGEFSCVLPGYVRFGPDIRLFQSSVKIRLMRGGIQVR
EKEAQANDSYKHAMGSVIMALGKGDKVWLESKLKGTESEKGITHIVFFGYLLYGK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic Sciences, Kitasato University, Laboratory of Molecular Biology; 1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408, Fax:0427-78-9403)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
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Takamatsu, N., Ohba, K., Kondo, J., Kondo, N. and Shiba, T.
Takamatsu, M., Ohba, K., Kondo, J., Kondo, N. and Shiba, T.
Takamatsu, M., Ohba, K., Kondo, J., Kondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Sondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J., Nondo, N. and Shiba, T.

Takamatsu, M., Sondo, J., Nondo, J.

Takamatsu, M., Sondo, J.

Takamatsu, M., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMSHP25 2005 bp mRNA linear ROD 03-FEB-19
Tamias asiaticus mRNA for HP-25, complete cds.
D12975
D12975.1 G1:287469
HP-25; collagen-like domain; hibernation-related protein; plasma
384 GCCTTTGCTGTGAAGCTGAGTGAACGCCCCCAGAGCCCTTCCAGCCCATTGTCTTCAAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATACAGGAGAAATAAGTGAAAATGACAAA---ATGCCCCTGTCCTGATATAGAAAGGTCA 126
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Tamias asiaticus liver cDNA to mRNA, clone:pCM25-3.
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Pred. No. 7.6e-14;
0; Mismatches 150;
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/db_xref="taxon:64680"
/clone="pcM25-3"
/fissue_type="liver"
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1983. .1988
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llarity 54.9%;
Conservative (
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Takamatsu, N.
Direct Submission
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/note="MER5A repeat: matches 26. .187 of consensus"
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                                                                                                                                                                                                                                                                                                       sapiens
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AUTHORS
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KEYWORDS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-AUG-2001) Nobuhiko Takamatsu, Kitasato University, Department of Bloschences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:takamatu@jet.sci.kitasato-u.ac.jp, Tel:81427789408,
                               444 GAGGCTCTGTACAATCAGGAGGGCCACTTCAACATGGCCACGGGAGAGTTCAGCTGTGTC 503
                                                                                504 CTCCCTGGTGTGTACAATTTTGGCTTTGACATTCGACTGTTTCAGAGATC 563
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                                                                                                                                                                                                                                                   Callosciurus caniceps HP-25 pseudogene, exon 3, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(AB067813.1:1503. .1658,AB069678.1:26. .185,39.
/gene="HP-25"
 247 GTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 GGACATCCAGGTATACCAGGAAGGCCAGGATGACGAGGCCCTCCTGGAGACATGGAGACG
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/clone="lambda Ts25G1"
join(AB067813.1:1503. .1658,AB069678.1:26.
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Callosciurus caniceps
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The tree squirrel HP-25 gene is a pseudogene
Eur. J. Biochem. 268 (22), 5997-6002 (2001)
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Pred. No. 1.5e-09;
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                                                                                                                          307 TGCCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAA 345
                                                                                                                                                       564 AGGCTCATGAGGGATGGTATCCAGGTCAGAGAAGAA 602
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39. .>559
                                                                                                                                                                                                                                                                  AB069679
AB069679.1 GI:18149913
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Best Local Similarity 55.5%;
Matches 156; Conservative
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128 c
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Takamatsu, N.
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AB067813S3
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187
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Lubraticad (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, Cabonitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clonerequest@sanger.ac.uk

On Dec 13, 1999 this sequence version replaced gl:3164067.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL: Sw:, SWISSPROT: Tr:, TREMBL: WP:, WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/HGP/Chr21

RPI-302D9 is from the library RPCI constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further worm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ньзигру 145880 bp DNA linear PRI 12-DEC-1999
Human DNA sequence from clone RP1-302b9 on chromosome 22 Contains
GSSs, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145880)
                                                                                                                           152 GGGTCCTTCCAGCCCATCATATTCAAGGAGTCTCTGTACAACCGGGAGGACCACTATAAC 211
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/note="MER3 repeat: matches 1. .144 of consensus"
783. .938
                                                                                220 GAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTT
                                                                                                                                                                                                                                                                                     272 GGACTGTTTCAGAGTTCTGTGAAGATAAGTCTCATGAGGAA 312
                                                                                                                                                                                                                                          280 GAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAA 320
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/organism="Homo sapiens"
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/chromosome="22"
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/clone_lib="RPCI-1"
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10331336 /note-"Alusp repeat: matches 1299 of consensus" 14501583 /note-"MIR repeat: matches 24160 of consensus" 16871752	/note-"L2 repeat: matches 25932661 of consensus" 23502660 26642981 /note-"Alusg repeat: matches 2300 of consensus" 7note-"Alusg repeat: matches 2300 of consensus" 7note-"MLTIE repeat: matches 116136 of consensus" 33443652 /note-"MLTIE repeat: matches 1309 of consensus"	repeat: matches 136359 of consenrepeat: matches 3364 of consensurepeat: matches 359568 of consenrepeat: matches 1311 of consensurepeat: matches 123 of consensurepeat: matches 123 of consensurepeat: matches 123 of consensurepeat: matches 123 of consensus	matches 1302 of consensus: matches 2377 of consensus: matches 9290 of consensus: matches 1295 of consensus atches 15532706 of consensus natches 91262 of consensus natches 15144 of consensus" natches 3161 of consensus"	/note="MSTB repeat: matches 2425 of consensus" complement(10179. 10678) complement(10179. 10678) note="match: GSS: En:B56592" complement(1020410728) /note="match: GSS: En:A0701486" complement(1024910706) /note="match: GSS: En:A0725495" /note="match: GSS: En:B4024" /note="match: GSS: En:B14024" /note="match: GSS: En:B14024" /note="match: GSS: En:B14024" /note="match: GSS: En:B14056" /note="match: GSS: En:B14050" /note="match: GSS: En:G19301"	13311339/ /note="MIR repeat: matches 174244 of consensus" 1339813698 /note="AluSp repeat: matches 1302 of consensus" 1369913810
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Complement(18872. 19230)

/note="match: GSS: Em:AQ005063"
/note="match: GSS: Em:B14179"
/note="match: GSS: Em:B14179"
/note="HENVH121 repeat: matches 4657. .5784 of consensus"
/note="HENVH121 repeat: matches 4657. .5784 of consensus"
/note="1" copies 2 mer ta 68 conserved"
/note="7" copies 2 mer tt 70 conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18393. 18712
//note="AluJb repeat: matches 1. 311 of consensus"
18713. 1913
//note="MER66-internal repeat: matches 4548. 4919 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anote="MSTA repeat: matches 2. .29 of consensus" 18324. .18392
Anote="MER66-internal repeat: matches 4919. .4993 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="THELB repeat: matches 1. .364 of consensus" 22302. .2537
/note="MER66-internal repeat: matches 2186. .2417 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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/note="MER66-internal repeat: matches 3017. .3102 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /noce="match: GSS: Em:AQ553482"
14616. 15060
/note="match: GSS: Em:AQ370601"
/note="match: GSS: Em:AQ370601"
/note="MIR repeat: matches 49. .233 of consensus"
15071. 15188
/note="L2 repeat: matches 2112. .2239 of consensus"
15304. 15399
                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 141. .225 of consensus"
14589. .14679
//note="MIR repeat: matches 173. .262 of consensus"
14597. .15201
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18296. .18323
/note="MIR repeat: matches 76. .174 of consensus"
13806. .13919
                                                                                                                                                                      /note="MIR repeat: matches 24. .142 of consensus"
14061. .14367
                                                                                                                                                                                                                                /note="AluY repeat: matches 1. .301 of consensus"
14368. .14452
                                                                                                       matches 77. .189 of consensus"
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                                                                                                /note="MIR repeat:
13945. .14060
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120 AAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTTCCAAGCCCCATCAT 179

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27067. .27138
/note="Charlie4 repeat: matches 1902. .1961 of consensus"
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/note="LiMD2 repeat: matches 5142. .5259 of consensus"
2760. .3005
/note="LiMD2 repeat: matches 5259. .6173 of consensus"
3418. .3477
                                                                                                                                                                                                                                                                                                                                                    3763. .4128
/note="MER82 repeat: matches 1. .386 of consensus"
3879. .4353
/note="match: GSS: Em:AQ559531"
4364. .4569
/note="L2 repeat: matches 2535. .2750 of consensus"
4612. .4930
/note="AluJo repeat: matches 1. .307 of consensus"
4934. .5220
/note="AluSx repeat: matches 1. .287 of consensus"
                                                                                                                                                                                                                                                             .4173 of consensus"
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/note="AluYb8 repeat: matches 1. .306 of consensus"
note="AluJb repeat: matches 1. .126 of consensus" 758. .1385
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21369. .21551
7.note="MIR repeat: matches 2. .187 of consensus"
22494. .22667
7.note="MIR repeat: matches 35. .236 of consensus"
23443. .23755
7.note="Alusx repeat: matches 1. .312 of consensus"
24052. .24348
7.note="Alusy repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7573. 7749
/note="MIR repeat: matches 22. .207 of consensus"
10322. 16495
/note="LIPA2 repeat: matches 7. .6146 of consensus
16265. .16787
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/note="MIR repeat: matches 20. .216 of consensus"
27067. .27138
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/note="match: GSS: Em:AQ557814"
5417. .5569
/note="MIR repeat: matches 2. .167 of consensus"
5645. .5708
/note="32 copies 2 mer at 71 conserved"
                                                                                                        .3716 of
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/note="match: STS: Em:G03694; match: STS:
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/note="16 copies 3 mer taa 97 conserved"
complement(5266. .5727)
                                                                                                                                                                                                                    3418. 3477
/note="30_copies 2 mer ac 90 conserved"
                                                                                                        /note="L1P repeat: matches 3221.
                                       758. .1385
/note="LiP_repeat: matches 3548.
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/note="24 copies 2 mer ac 77
                                                                                   1374. .1869
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The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep CTA-732E4 is from the human BAC library described in U-J. Kim et al. (1996)
                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone CTA-732E4 on chromosome 22q12.1 Contains ESTs, STSs and GSSs, complete sequence.
ALO08722.16 GI:5419644
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone CTA-732E4 The true left end of clone RP11-54116 is at 5510 in this sequence. The true right end of clone CTA-544A11 is at 41939 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08 DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone.

On Jul 8, 1999 this sequence version replaced gi:5304865.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known amontated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was generated from part of bacterial clone contigs Muman chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
           90759 CTGTACCATCCCTAGTGTGTGTGTTTTGAATTTGAGCTGTTTCAGAGCTGTGC 90700
                                                                                                                      90819 CITCAAGGAAGCCCITIAIAAIACICAGIICCAIIICCAITICICIGGGAAGGAIICAC 90760
                                                                                                                                                                   240 TIGCAGGIGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGGTGCATCATTGCAAGGT 299
                                                                               180 CTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGAGTCTTTGC 239
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/note="LiM1 repeat: matches 994. .1640 of consensus"
632. .757
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/clone_llb="CIT978SK-A2"
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/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                  90699 AAATGTGGGTATTATGAGGAA 90679
                                                                                                                                                                                                                                                           GAATATTTGGCTAATGAGGAA 320
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Complement(41368. 41893)

/note="match: GSS: Em:B18147"

/note="match: GSS: Em:B18147"

/note="match: GSS: Em:B18147"

/note="match: GSS: Em:B18193)

/note="match: GSS: Em:B18193)

/note="match: GSS: Em:B18193]

/note="match: GSS: Em:B18191; match: STS: Em:B14391"

/note="LTS repeat: matches 2540. .2659 of consensus"

/note="LIMI repeat: matches 2469. .4924 of consensus"

/note="LIMIS repeat: matches 2409. .4924 of consensus"

/note="LIMIS repeat: matches 2409. .472 of consensus"

/note="LIMIS repeat: matches 2400. .472 of consensus"
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40551. 40904
7. Orde="THELB repeat: matches 3. .364 of consensus"
40905. 41859
7. Note="TIGGER1 repeat: matches 1394. .2418 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6166 of consensus"
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3371. .34072
/note="Alu3o repeat: matches 1. .310 of consensus"
/note="Match: GSS: Em:AQ407436"
3716. .38583
/note="TGGER repeat: matches 2. .1394 of consensus 38584 .38937
/note="THE1B repeat: matches 3. .364 of consensus 38938 .40548
/note="THE1B-INTERNAL repeat: matches 1. .1580 of cote="THE1B-INTERNAL repeat: matches 1. .1580 of
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/note="FLAM_A repeat: matches 81. .133 of consensus"
48061. .48341
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49916. 50351
/note="match: GSS: Em:AQ805065"
50076. 50449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 1072. .1341 of consensus" 32884. .32952
/note="MRR45B repeat: matches 2. .76 of consensus" 313181. .33436
/note="MRR45C repeat: matches 676. .952 of consensus" 33504. .33671
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48399. .48549
40002-"FRAM repeat: matches -5. .146 of consensus"
49002. .49450
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/note="55 copies 2 mer ag 67 conserved"

47276. .47434

/note="MBESA repeat: matches 4. .189 of consensus"

47698. .47991

/note="Aluss repeat: matches 1. .299 of consensus"
                                             .2744 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .364 of consensus"
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/note="L1MB5 repeat: matches 5157. .6166 of conser 31294. 31449
/note="L1MB2 repeat: matches 5991. .6146 of conser 31344. 31681
/note="MIR repeat: matches 93. .254 of consensus" 31914. .32062
                                                                                                                                                                                                                                                                                                                                                                                                          .4984 of
                                                                                                                       /note="10 copies 4 mer tata 87 conserved" 28759. 28798
/note="20 copies 2 mer at 87 conserved" 29334. 29421
/note="22 copies 4 mer gaaa 65 conserved" 29805. 30155
/note="LIMBS repeat: matches 4639. 4984 of the copies 4639 o
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                  2 repeat: matches 2683.
28797
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Unpublished

Birren, L. Minton, L., Nusbeum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhajter, B., Choses, I. to 13580)

Birren, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhajter, B., Choepel, Y., Colangelo, M., Callins, S., Collymore, A., Cook, A., Cook, A., Cook, A., Cook, A., Gorton, D., Harden, J., Garaero, B., Gord, S., Goyette, M., Graham, L., Grand-Pterre, N., Gord, S., Goyette, M., Graham, L., Grand-Pterre, I., Johnson, R., Jones, C., Kamat, A., Harton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartass, A., Kells, C., LaRocque, K., Manthas, C., Macdonald, P., McGarthy, M., McEwan, P., McGarthy, M., McEwan, C., Macdonald, P., Morcarthy, M., McEwan, C., Macdonald, P., Morcarthy, M., McEwan, C., Madonald, P., Morcarthy, M., McEwan, C., Macdonald, P., Morcarthy, M., McEwan, C., Madonald, P., Marter, M., Riley, R., Stanger, M., Najlor, C., Noran, C., McGarthy, M., Milley, R., Santos, R., Stanger, P., Okneil, D., Okneil, D., Okneil, D., Okneil, R., Wold, M., Willey, R., Stanger, M., Stanger, C., Schupback, R., Stanger, McMan, J., Zengely, P., Stenet, Camarts, M., Tarigillo, J., Vassillev, H., Viel, R., Wold, M., Wull, M., Wann, D., Ye, W. J., Young, G., Johnster, B., Nusbaum, C., Lamer, A. and Zody, M. Ye, W. J., Young, G., Marten, M., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhquer, B., McCarthy, M., Berreitz, P., McGarthy, M., Gage, D., Galagan, J., Chang, J., Chang
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   Length 90497;
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Homo sapiens chromosome 8, clone CTD-2384G12
Unpublished
Score 63.4; DB 9;
Pred. No. 8.1e-08;
); Mismatches 21;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published only in Database (2002)
2 (bases 1 to 51000)
4 tattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Bulict Submission
Submitted (24-MAY-2002) Masahira Hattori, The Institute of Physical
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Homo sapiens genomic DNA, chromosome 18, clone:RP11-78F17, complete
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             Direct Submission
Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 18, 2002 this sequence version replaced gi:21699681.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 13580: contig of 13580 bp in length.
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                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L22077
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Pred. No. 8.4e-08;
0; Mismatches 11;
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42430 a 25457 c 25972 g 42021 t
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/db_xref="taxon:9606"
/chromosome="8"
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Zembek, L., Zimmer, A. and Zody, M.
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AP005265.2 GI:21328206
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86.4%;
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Matches 70; Conservative
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Homo sapiens chromosome 18 clone RP11-78F17 map 18, WORKING DRAFT
SEQUENCE, 36 unordered pieces.
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-845-533-911, Fax:81-45-503-9170)
On Jun 6, 2002 this sequence version replaced gi:21218138.
Location/Qualifiers
1. 51000
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-78F17
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Pred. No. 8.9e-08;
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9626 c 9391 g
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AC027433.2 GI:7677878
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                            Consensus quality: 124499 bases at least Q40 consensus quality: 133382 bases at least Q40 consensus quality: 133772 bases at least Q20 linsert size: 139000; agarose-fp linsert size: 141014; sum-of-contigs Quality coverage: 3.5 in Q20 bases; agarose-fp Quality coverage: 3.4 in Q20 bases; sum-of-contigs
                                                                               Center project Information
Center project name: L7820
Center clone name: 78 F.17
Center clone name: 78 F.17
Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.960731
                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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23095: contig of 1917 bp in length
23195: gap of 100 bp
25510: contig of 2315 bp in length
25610: gap of 100 bp
27999: contig of 2389 bp in length
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39922: contig of 2576 bp in length
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59485: contig of 4113 bp in length
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7426: contig of 24
7526: gap of 100
9699: contig of 21
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92295 92394; gap of
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 6, clone RP11-608N7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 133169 CCTAGAGATTTGTGAACTTTGAACCTGAAAGAGATGATTTAGAGTATCAGGGAAGAATT 133228
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Homo sapiens chromosome 6 clone RP11-608N7 map 6, WORKING DRAFT
SEQUENCE, 27 unordered pieces.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Best Local Similarity 74.1<sup>§</sup>
Matches 80; Conservative
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TITLE
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                             Center clone name: 608_N_7

Center clone name: 608_N_7

Sequencing vector: M13, M77815; 100% of reads
Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator B1g pye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 132985 bases at least Q40

Consensus quality: 140748 bases at least Q30

Consensus quality: 140748 bases at least Q20

Insert size: 138000; agarose-fp

Insert size: 138000; agarose-fp

Insert size: 36 in Q20 bases; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45639: contig of 4775 bp in length 739: gap of 100 bp 5882: contig of 5887 bp in length 5926: gap of 100 bp 56617: contin of for a
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contig of 1378 bp in length
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14633: contig of 2462 bp in length
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p of 100 bp
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102458 112952: conti
112953 113052: gap of
                                               Center project name:
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6853: co
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113053 124237: contig of 11185 bp in length 124238 124337: gap of 100 bp 125694: contig of 11357 bp in length 135695 133794: gap of 100 bp 135795 149038: contig of 13244 bp in length.
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ORIGIN
                                                                                                  source
                                                                               FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmailais Eutheria; Primates; Catarrhini; Hominidae; Homo.

Manmailais Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 162083)

Muzny,D.M., Adama,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Ate,J.R., Banks,T., Barbaria,J.,

Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brideva,M., Brown,E., Brown,M., Bryant,N.P., Bubay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.C.,

Carroll,J.C., Cardorly,J., Christopoulos,C., Cleveland,C.D., Cox,C.,

COyle,M.D., Dathorne,S.R., David,R., Davida,O.,

Denn,A.L., Dinny,Y., Dintstopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davids,O.,

Denn,A.L., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escottch,M., Palls,T., Perraguto,D., Flaggy,N., Fort,C.,

Coxter,P., Frantz,P., Gorrell,J.H., Guevara,W., Gunarenne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,R., Morris,R., Holloway,C.,

Jacobson,B., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,

Jacobson,B., Jia,Y., Man,U., King,L., Korvah,J.,

Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,

Kovar,C., Kratovic,J., Lulx., Ludker,J., Hultyks., Man,Dilvet,S.,

Lewis,L., Li,J., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M.,

Martines,E., Massey,E., Mawhiney,B., Martin,R., Martindale,A.,

Mayon,M., Newlonu,G., Orgaunye,N., Miner,Z., Mitchell,Y., Newtson,J., Newtson,N.,

Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,

Stone,H., Zutton,A., Savetk,A., Tabor,P., Tamerisa,A., Thomas,N.,

Thomas,S., Wallems,R., Wallers,R., Walledry,R., Wallenger,R., Wallenger,R., Wallenger,R., Rock,A., Tabor,P., Tanger,H., Sulled, M., Rolsson,B., Thomas,S., Wallenger,N., Wallerson,B., Tanger,H., Sulled, M., Wallerson,B., Wallerson,B., Tanger,R., Soott,G., Shen,H., Ston,H., Sulson,B., Tangel,H., Sulson,B., Palled,R., Sulson,B., Tangel,H., Sulson,B., Tangel,H., Sulson,B., Palled,R., Sulson,B., Tangel,H., Sulson,B., Tangel,H., Sul
                                                                                                                                                                                                                                                                                                                                                                      162063 bp DNA linear PRI 13-JUL-2001
Homosapiens 9 BAC RPI1-100N10 (Roswell Park Cancer Institute Human
AC015553
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Direct Submission
Submitted (17-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                289 CATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATT 348
                                                        ;
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Length 149038;
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Score 63.2; DB 2;
Pred. No. 9.7e-08;
0; Mismatches 28;
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Unpublished
2 (bases 1 to 162063)
16.0%;
illarity 74.1%;
Conservative
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                               Similarity
                                                     80;
     Query Match
Best Local (
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AC015553/c
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TITLE
JOURNAL
                                                     Matches
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AUTHORS
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37628 aggaaagaag(n)aaggaaggaa ccagcaataa(a)caagtagaagaa ccagcaataa(a)caagtaagaat 68252 gctggaattg(n)ctttafttt gctggaattg(l)ctttafttt 68273 catctaggtg(n)nggttccatg catctaggtg(c)tggttccatg catctaggtg(n)nggttccatg tccatggtg(c)tggttccatg tccatggtg(n)atacatgaat tccatggtg(n)atacatgaat tccatggtg(n)atacatgaat tccatggtg(n)atacatgaat tggtgataag(n)aacagaaga acttaggtg(n)atacatgaat tggtgataag(n)caacagaaga tggtgataag(n)caacagaaga acttagaacctag(c)caagtccc 113818 tactgaactcan(n)caaggtccc cgtaacttag(c)caaggtccc ggtaacttag(c)caaggtccc tgatactgaa(n)ccnctaaaaa tactgaaacc(a)ctaaaaaaa tactgaaacc(a)ctaaaaaaa tactgaaacc(a)ctaaaaaaa aaaaaaaaaaaaaaaaaaaaaaaaaaaa	# 350  bases 300  250  150  150  50  7	Version: 1.01 qxfo.  FEATURES Location/Qualifiers Location/Qualifiers   . 16208     . 16208     / Organism="Homo sapiens"     / Ab_xref="txxon:9606"     Ab_xref="txxon:9606"	repeat_region repeat_region repeat_region repeat_region repeat_region	ari
	CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.  ANNOTATION OF FEATURES:  STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.  Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.  Genes and Region of sequence similarity are identified by NIAST	(Nuc. Acids Res. 25:3389-3402) similarity (expect < 16-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice juuctions. Sequences that are not identical matches are annotated as similar. Sequences that are not standard of double strand coverage with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.	TYIDUAL BASES: This sequence meets stringe timated error rate less than 1 per 10,000 est quality individual bases and measures sted below. Description of the metrics ca/gc.bcm.tmc.edu:8088/quality.info/genbank	Contig length: Phrap values in estimate: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:  Number of N's in consensus changing edits

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VERSION

COMMENT

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101521 101650: gap of 100 bp 112967 112966: contig of 11346 bp in length 112967 113066: gap of 11346 bp in length 113067 119218 119317: contig of 6151 bp in length 119218 119317: gap of 100 bp 119318 121557 121656: gap of 100 bp 121557 121656: gap of 100 bp 121657 121656: gap of 100 bp 121657 134400: contig of 12344 bp in length 134401 134500: gap of 100 bp 134501 144934: contig of 10434 bp in length 144935 145034: gap of 100 bp 149318 149918: contig of 100 bp 149919 149918: contig of 3260 bp in length 148919 149919: contig of 3260 bp in length 152178: contig of 3260 bp in length 152178: contig of 3260 bp in length
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85: gap of 100 bp
92978: contig of 3093 bp in length
                                                                                                                                                            101520: contig of 3892 bp in length
                                                                                                contig of 4450 bp in length
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93079 97528: con
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Homo sapiens chromosome 9 clone RP11-1K21, *** SEQUENCING IN
PROCESS ***, 20 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                29373 ACTTTGAACTTGAGAGAGAGATTTAGGGTATGCCAGAAGAATTTCTAAGCAGCAAAGC 29314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9863606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGRP4, version 4.5
Sequencing vector: plasmid; L08752, 100% of reads
Chemistry: Dye-terminator Er-amersham; 24% of reads
Chemistry: Dye-terminator Er-amersham; 24% of reads
Consensus quality: 164370 bases at least Q40
Consensus quality: 166213 bases at least Q30
Consensus quality: 170527 bases at least Q30
Consensus quality: 170527 bases at least Q30
Insert size: 173234; sum-of-contigs
Insert size: 168172; 44% error; agarose-fp
Quality coverage: 4.13x in Q20 bases; sum-of-contigs Quality
                                                               ATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAAAGC 363
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19; Indels
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80131: contig of 13900 bp in length
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                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
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Mclay, K.
74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Caudmisted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquifies: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Jul 29, 2001 this sequence version replaced gi:15026899.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                              ;
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RP11-462B18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83975 ACTITIGAACTIGAGAGAGATGATITIAGGGTATGGCAGAAGAATTITCTAAGCAAGGC 83916
                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 ATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAAAGC 363
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 176932)
                                                                                                                                                                                                                                                                                        1906 others
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                                                              /note="assembly_fragment:01972"
152279. .165020
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fragment_chain:6
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Pred. No. 1.5e-07;
                         'note="assembly_fragment:01696"
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36761 c 35231 g 49719 t
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                                               148919. .15217B
.148818
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AL157884.9 GI:15029097
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79.6%;
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Best Local Similarity 79.6
Matches 74; Conservative
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Direct Submission
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Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hygienic
Sciences, Kitasato University, Laboratory of Molecular Biology;
11-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
Fax:0427-78-9403)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takamatsu, N., Ohba, K., Kondo, J., Kondo, N. and Shiba, T.
Hibernation-associated gene regulation of plasma proteins with a collagen-like domain in mammalian hibernators
MOI. Cell. Biol. 13 (3), 1516-1521 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D12976.1 GI:287471
HP-27; collagen-like domain; hibernation-related protein; plasma
This sequence is the entire insert of clone RP11-462B18 The tru right end of clone RP11-555J4 is at 30638 in this sequence. The true right end of clone RP11-1K21 is at 97783 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 ATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAAAGC 363
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Tamias asiaticus mRNA for HP-27, complete cds.
D12976
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Pred. No. 1.5e-07;
0; Mismatches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89890 ATTCAAGAGGTGACTTGGGTGCTGTTAAAGACA 89858
                                                                                                                                                                                                                                                                                                   /evidence=not_experimental 54421 a 37529 c 35943 g 49039 t
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76326. .77014
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                                                                        Location/Qualifiers
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79.6%;
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                                                                                                    Gaps
                                                         Query Match Best Local Similarity 55.6%; Pred. No. 1.2e-07; Matches 120; Conservative 0; Mismatches 96; Indels 0;
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/product="HP-27"
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0 0 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		) 000000 000000000000000000000000000000	RESULT 1 BE121287/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT
5.1.3 Compugen Ltd. Search time 262.925 Secontinous alignments)		ters: 32308132			Score distribution.     Description
GenCore version Copyright (c) 1993 - 2003 OM nucleic - nucleic search, using sw model Run on: February 19, 2003, 23:48:42;	Title:  US-09-997-610-1_COPY_53_156  Perfect score: 104  Sequence:  Scoring table: IDENTITY_NUC  Gapop 10.0 , Gapext 1.0  Searched: 16154066 seqs, 8097743376 res	mber of hits satisfying chosen par DB seq length: 0 DB seq length: 2000000000 cessing: Minimum Match 0% Maximum Match 100% Tisting first 45 summaries	Database: EST:*  EST:*  1: em_estban:*  3: em_esthum:*  4: em_estn:*  5: em_estor:*  6: em_estpl:*  7: em_estro:*  9: qb_est1:*  11: qb_htc.*		Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score diamond is derived by analysis of the total score diamond.  Result  No. Score Mutch Length DB ID  C 1 38.4 36.9 531 10 BE121287  2 38 36.5 483 13 B132379  3 36.8 35.4 695 10 BE285930  6 36.8 35.4 776 13 B1554667

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// Crganisme"Rattus norvegicus"
// Straine"Spraque-Dawley"
// Straine"Spraque-Dawley"
// Ab_Arsef="taxon:10116"
// Alone="UI-R-CAO-baw-b-08-0-UI"
// Alones="UI-R-CAO-baw-b-08-0-UI"
// Alone="UI-R-CAO"
// Alone="Vector: pT773-D-Rac (Pharmacia) with a modified
// Anote="Vector: pT773-D-Rac (Pharmacia) with a modified
// Anote="Vector: pT773-D-Rac (Pharmacia) with a modified
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McCarter Parastrongyloides trichosuri cDNA 5' similar to TR:Q61436
Q61436 PROCOLLAGEN, TYPE IV, ALPHA 5 ;contains element PTR5
B1322379
tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clonne distribution: clones will be available through seq primer: MI3 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site at ratest.eng.ulowa.edu. The subtraction has be previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
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Pred. No. 2.5;
0; Mismatches
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TAG_SEQ-CTAGG"
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
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62.5%;
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BI322379
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The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Seq primer: -40RP from Glaco High quality sequence stop: 428.
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was mader by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR CDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. Warwick Grant of AgRearch, New Zealand
(warwick grantleggresearch.co.nz)."
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylle, T., Dante, M., Marra, M., Hiller, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                              /clone_lib="Parastrongyloides trichosuri FL pAMP1 v1
Chiapelli McCarter"
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Contact: McCarter JP
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1810
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
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    .483
/organism="Parastrongyloides trichosuri"
/db_xref="taxon:131310"

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/lab_host="DH10B"
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  est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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BI863711.1 GI:16005501
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Email:
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/lab_host="Peree Living"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CONA was made by using Dynabead oliqo-dT priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR cDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. Warwick Grant of AgRearch, New Zealand
(warwick grant@agresearch.co.nz)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 889)
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
                Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1. 552
/organism="Parastrongyloides trichosuri"
//db_tref="taxon:131310"
/clone_lib="Parastrongyloides trichosuri FL pAMP1 v1
Chiapelli McCarter"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:10090"
/clone="IMAGE:6395968"
/clone=lib="NCI_CGAP_CC24"
/lab_host="DH10B (TI phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.5%; Score 38; DB 1
62.8%; Pred. No. 3.2;
iive 0; Mismatches
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Plate: LLAM13891 row: h column: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Location/Qualifiers
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Matches 59; Conservative
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connect Access Strangers, Strangers 
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                                                                                                                                                                                                                                                                                                          36.0%; Score 37.4; DB 14; Length 889; illarity 61.5%; Pred. No. 4.6; Conservative 0; Mismatches 37; Indels 0
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/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 97
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Pred. No. 6.7;
0; Mismatches
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High quality sequence stop: 553.
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/db_xref="taxon:10090"
/clone="IMAGE:3496499"
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1. .695
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61.5%;
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BE285930
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Matches 59; Conserv
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237 GTCCCAGGACAAACCGGAGGA 257
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Caenorhabditis elegans.
Caenorhabditis elegans
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Matches 53; Conserv
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/strain="129,C57BL/6J,FVB/N"
/db_aref="taxon:10090"
/clone="Inb="NCI_CGAP_Mam3"
/clone="Inb="NCI_CGAP_Mam3"
/tissue="type="tumor, gross tissue"
/dev_stage="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH108"
/note="Organ: mammary: Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999).
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D69730
D69730.1 GI:1105372
                                                                                                                                                  BI554667 776 bp mRNA linear EST 05-SEP-2001 603236619F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5289605 5',
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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lnl.gov

Plate: LLAMI132 row: f column: 06

High quality sequence stop: 759.
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Pred. No. 6.7;
0; Mismatches 37;
                                 316 TCCCAGGTTCTAAAGGTGAAATGGGTGTCATGGGAA 351
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             62 TACCACAATATACAGGAGAAATAAGTGAAATGACAA
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1. .776
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BI554667
BI554667.1 GI:15441981
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61.5%;
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BI554667
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BJ136441 unpublished oligo-capped cDNA library, C. elegans L1 stage Caenorhabditis elegans cDNA clone ykll13b05 3', mRNA sequence.
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Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota: Metazoa: Nomatoda: Chromadorea: Rhabditida; Rhabditoidea
: Rhabditidae: Peloderinae; Caenorhabditis.
1 (bases I to 632)
Kohatra.Y., Shin-i.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
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/db_xxref="taxon:6239"
/db_xxref="taxon:6239"
/clone="kill13005"
/clone=lib="unpublished oligo-capped cDNA library, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 360;
                                                                                                                                     Toward an expression map of the C.elegans genome Unpublished (1994)
Contact: Yuji Kohara
Genome Blology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Far: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk/3c7"
/clone="lib""Yuji Kohara unpublished cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
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    632
/organism="Caenorhabditis elegans"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
116 c 105 g 42 t
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608 GCCCCAGGACAATCCGGAGGA 628
                                                  61 TTACCACATATACAGGAGAA
                                                                                                                                                                                                                                                   sequence.
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BI323061
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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1 (bases 1 to 726)
Kohara; Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
                        /tissue_type="https://dev.stage="till"
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/dev.stage="till"
/note="The AD-wincDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

163 c 214 g 175 t 5 others
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/dev_stage="L1"
/dev_stage="L1"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
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                                                                                                                                                                                                                                                   0; Gaps
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/clone_lib="unpublished oligo-capped cDNA library,
elegans L1 stage"
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                                                                                                                                                                                                            Score 36.2; DB 13; Length
Pred. No. 9.6;
0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A complementary view of the C.elegans genome Unpublished (2002)
Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshinlegenes.nig.ac.jp.
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219 c 192 g 125 t
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Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="N2"
/db_xref="taxon:6239"
              /sex="hermaphrodite"
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BJ108893.1 GI:18268921
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Caenorhabditis elegans
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                                                                                                                                                                                                             34.8%;
65.4%;
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65.48;
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les 53; Conservative
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Matches 5
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Matches
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BJ108893
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1 GCTGGACCTCCAGCACCCCCAGAGGAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGT 60

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McCarter.

/dev_stage="L2"
/lab_host="DH10B"

/lab_host="DH10B"

/note="Vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The CDNA was made by using
University, St. Louis. The CDNA was made by using
Dynabead oligo-dr priming (Dynal). PCR based library
using a modified protocol from the SWART PCR CDNA
Synthesis Rit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."

85 c 94 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The library was constructed by Brandi Chiapelli and Dr. James McCarter (briapellewatson.wustl.edu & jmccartee@watson.wustl.edu washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 392.
                                                                                                                                                                                                                                                  ö
                 kt68h01.yl Strongyloides ratti L2 pAMP1 vl Chiapelli McCarter
Strongyloides ratti CDNA 5' similar to TR:Q19079 Q19079 COSMID
EGAP7. [1] ;contains element MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Strongyloides ratti"
/db_xref="taxon:34506"
/clone_lib="Strongyloides ratti L2 pAMP1 v1 Chiapelli
McCarter"
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Unpublished (1999)
Contact: McCarter JP
Contact: McCarter JP
Mashington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: est@watson.wustl.edu
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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461 bp
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                                                                                                                   BI323061
BI323061.1 GI:15002247
                                                                                                                                                                                           Strongyloides ratti.
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Matches 54; Conserv
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Page

DEFINITION

RESULT 11 BG310518

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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/organism="Strongyloides stercoralis"
/strain="Filariform larvae obtained from humans"
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/db_host="xbn9574"-SSFH"
/lab_host="xbn1 Blue MRF" (Stratagene)"
/note="vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
/note="vector: Lambda Uni-ZAP XR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BES80165 468 bp mRNA linear EST 09-MAY-2001 kg37h09.yl TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to TR:P79758 P79758 COLLAGEN ;contains TAR1.t3 TAR1 repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                  BE029138 287 bp mRNA linear EST 09-MAY-2001 kp25d01.yl TBN95TM-SSFH Strongyloides stercoralis cDNA 5' similar to WP:W01B6.7 CE03759 COL-2: CUTICLE COLLAGEN 2 ; contains element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NaID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
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Strongyloides stercoralis
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 CCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCC 104
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                                                                                                                                                                           MSR1 repetitive element ;, mRNA sequence.
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59.4%; Pred. No. 15;
live 0; Mismatches
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1. .287
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BE029138.1 GI:8322600
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BE580165
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tes 60; Conserv
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BE580165
      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="molting L3"
/dev_stage="molting L3"
/lab_host="Yall-Blue MRF"
/note="vector: Lambda Uni-ZaP XK; Site_1: Eco RI; Site_2:
/note="vector: Lambda Uni-ZaP XK; Site_1: Eco RI; Site_2:
Xho I; Filatial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0, volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I: The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 1086 independent
recombinants and the average insert size is -1200 bp. The
                                                                                                                                                                                                BG310518 672 FEB-2001
SWOv3MCAM56C07SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM56C07 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 t
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1. .675
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BG310518.1 GI:13112376
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157 c 1
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Matches 55; Conservative
                                                                                                                                                                                                                                                                                                         mRNA sequence.
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                      1 (bases 1 to 468)
MCGARTER_J. Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
Clifton,S., Chiapelli,B., Franklin,C., Theising,B., Bowers,Y., Glbbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Magnire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey, N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
Tha Library was constructed by Dr. Thomas Nutman and Nature of
MalD, Will (fuutman@nli.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 325.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Strongyloides stercoralis"
Strain="Rabbditiform larvae obtained from gerbils"
/db.xref="taxon:6248"
/clone_lib="TBN95TM-SSR"
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Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Panagrolalmoidea, Strongyloididae, Strongyloides.
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Pred. No. 18;
0; Mismatches 33;
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92 c 134 q
                                               Strongyloides stercoralis.
                                                                      Strongyloides stercoralis
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    BE580165.1 GI:9831107
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Best Local Similarity 62.5%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: McCarter JP
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/organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/db.rafe="texaon:6248"
/clone_lib="TBN95TM-SSR"
/db_host="XL-1 Blue MRF" (Stratagene)"
/note="Wector: Lambda Uni-2AP XR (Stratagene); Site_l:
ECORI: Site_2: xhoi; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the EcoRI site to the Xhoi site. The library
has an unamplified titer of 1 x 10E5 pfuvml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700)."
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BE286914
1 (bases 1 to 483)
MCGATLER, J. CLIfton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.
Catter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.
Dante, M., Marra, M., Hillier, L., Franklin, C., Tsagareishvili, R., Rohndoy, S., Magulfre, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutmanenih.gov). DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
High quality sequence stop: 432.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 GGACCACCAGGACAAGATGGATCTCCAGGAGAACAAGGACCAGAAGGTGAAGGTTTA 82
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                                                                                                                                                                                                                                                               The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkay, Box 8501, St. Louis, MO 63108, USA
The: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 g
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov.h column: 19

High quality sequence start: 9

High quality sequence start: 9

High quality sequence stop: 604.

Location/Qualifiers

I. 814

/ Corganism="Max musculus"
/ strain="C57BL/G"
/ db.zef="taxon:10090"
/ clone="IMAGE:3487170"
/ clone="IMAGE:3487170"
/ clone="IMAGE:3487170"
/ clone="IMAGE:3487170"
/ clone="Lub" NCI_CGAP_Mam5"
/ tissue_type="tumor, gross tissue"
/ dev_stage="T, months"
/ lab_host="Dig an mammary; Vector: pCMV-SPORT6; Site_I: SalI;
Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies: Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

212 ...

NIH.

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NIH.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 97
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Matches 58; Conserv
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 53; Conserv
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                                      SEQ ID NO 20
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Sequence 635, App
Sequence 647, App
Sequence 624, App
Sequence 624, App
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Sequence 63, App
Sequence 63, App
Sequence 15, Appli
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Sequence 15, Appli
Sequence 3, Appli
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Sequence 2, Appli
Sequence 11, Appl
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Sequence 7, Appli
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4645.518 Million cell updates/sec
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                                                                                                                 February 19, 2003, 16:09:30; Search time 6.86562 Seconds
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11. /cgn2_6/ptodate/2/ina/5A_COMB.seq:*
22. /cgn2_6/ptodate/2/ina/5B_COMB.seq:*
33. /cgn2_6/ptodate/2/ina/6A_COMB.seq:*
44. /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
55. /cgn2_6/ptodate/2/ina/FUCLCS_COMB.seq:*
66. /cgn2_6/ptodate/2/ina/FUCLCS_COMB.seq:*
70012_6/ptodate/2/ina/FUCLCS_COMB.seq:*
70012_6/ptodate/2/ina/PacKfilesL.seq:*
70012_6/ptodate/2/ina/FilesL.seq:*
70012
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-342-661C-1
US-08-159-784-4
US-08-342-411A-1
US-08-383-744-1
US-08-999-336-1
US-08-999-336-1
US-09-134-001C-635
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US-09-134-001C-624
US-09-134-001C-693
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US-09-439-856-2
US-08-555-669-11
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5510466-1
US-08-494-168-1
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Maximum Match 100%
Listing first 45 summaries
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104
                                                                             nucleic search, using sw model
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Match Length DB
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APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978
CURRENT FILING DATE: 1999-06-29
PRIOR PRICATION NUMBER: 60/092,279
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
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     Sednence Sed
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US-09-029-348-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1881;
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Pred. No. 0.088;
0; Mismatches 33; Indels
US-09-073-663-11

PCT-US94-12883-3

US-09-125-58-3

US-09-067-351-5

US-09-126-1351-5

US-09-126-111A-15

US-08-948-22-3

US-08-948-22-3

US-08-948-22-3

US-08-97-1145-3

US-08-97-117-1

US-08-128-117-1

US-08-128-117-1

US-08-128-117-1

US-08-128-117-1

US-08-128-117-1

US-08-128-118-1

US-08-128-1

US-08-128-1

US-08-154-365-1

US-09-291-839-1

US-09-291-839-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER TITLE OF INVENTION: NOVEL PROCOLLAGENS FILE REFERENCE: d087857PUS LISTING CURRENT APPLICATION NUMBER: US/09/029,348 CURRENT FILING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 20 SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 CTCCAGGACCTCCTGGTGCTATAGGT 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 20, Application US/09029348; Patent No. 6171827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-342-681C-7
; Sequence 7, Application US/09342681C
; Patent No. 6355782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.9%; Sccilarity 61.6%; Pre
Conservative 0;
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TELEPHONE:
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US-08-159-784-4
 SEQ ID NO 1
LENGTH: 1574
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US-08-159-784-4
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Sequence 14, Application US/09342681C
Sequence 14, Application US/09342681C
Sequence 14, Application US/09342681C
Sequence 153782
Sequence INFORMATION:
TATLE ON INVERTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978
CURRENT APPLICATION NUMBER: US/09/342,681C
CURRENT FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Hypohydrotíc ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978
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                                                                                                        Score 30.4; DB 4; Length 821; Pred. No. 0.54;
                                                                                                                                           31; Indels
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                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                         378 TCCTGGAATTCCAGGAACAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 TCCTGGAATTCCAGGAACAA 634
                                                                                                        29.2%;
61.2%;
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illarity 61.2%;
Conservative
                                                                                                                                           49; Conservative
                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-681C-7
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; LOCATION: (1)..(1176)
US-09-342-681C-14
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
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LENGTH: 1176
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SEQ ID NO 7
LENGTH: 821
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                                                                                                                                  Length 1574;
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 30.4; DB 1; ilarity 71.4%; Pred. No. 0.89; Conservative 0; Mismatches 16;
                                                                                                                                  DB 4;
                                                                                                                                Query Match 29.2%; Score 30.4; DB Best Local Similarity 61.2%; Pred. No. 0.68;
                                                                                                                                                                    0; Mismatches
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APPLICATION NUMBER: US/08/159,784 FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION INFORMATION:
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(617) 542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      49; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                     ; NAME/KEY: CDS
; LOCATION: (242)..(1417)
US-09-342-681C-1
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 40; Conserva
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STATE: Massach
COUNTRY: U.S.A
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STREET: One Liberty Place, 46th floor CITY: Philadephia
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Best Local Similarity 66.15
Matches 41; Conservative
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; LOCATION: 331..1602
US-08-383-744-1
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MOLECULE TYPE: CDNA
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CLASSIFICATION:
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                                                                      19103
                      CITY: Ph
STATE: P
COUNTRY:
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| 730 GA 731
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Patent No. 5702948
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Davis, James G.
TITLE OF INVENTION: Saccular collagen and Compositions
TITLE OF INVENTION: and
TITLE OF INVENTION: Methods for Making and Using the Same NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/342,411A
FILING DATE: 18 NOV-1994
CLASSIFICATION: 435
ATTORNEY APPLICATION: 435
                                                                                 GENERAL INFORMATION:
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
ITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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                                                   Sequence 1, Application US/08342411A Patent No. 5639616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
REFRENCE/DOCKET NUMBER: ARCD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 base pairs
                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STRANDEDNESS: single
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; LOCATION:
US-08-342-411A-1
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ADDRESSEE:
                               US-08-342-411A-1
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APPLICANT: Davis, James G. .
TITLE OF INVENTION: Saccular collagen and Compositions
TITLE OF INVENTION: and Methods for Making and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1839;
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STREET: One Liberty Place, 46th floor
CITY: Philadephia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Score 28.4; DE 66.1%; Pred. No. 3.2; tive 0; Mismatches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,744
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Thu Feb 20 14:55:01 2003

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Pred. No. 3.2;
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GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Davis, James G.
TITLE OF INVENTION: Saccular collagen and Compositions and
TITLE OF INVENTION: Methods for Making and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Woodcock Washburn Kurtz Macklewicz & Norris
: One Liberty Place, 46th floor
Philadephia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                         ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2653
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/383,744
FILING DATE:
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APPLICATION NUMBER: US 08/383,744
FILING DATE: 02-FEB-1995
CLASSIFICATION:
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                                                                                                                                                                                                                                       LENGTH: 1839 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
; LOCATION: 331..1602
US-08-999-336-1
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Matches 41; Conserva
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CLASSIFICATION:
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PCT-US96-01427-1
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 635
LENGTH: 390
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                            28 CCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGTT 61
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0
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0
                                                                                                                                                                                                                         Length 1839;
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                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                       Score 28.4; DI
Pred. No. 3.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 28.2; Di 57.3%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 1997-08-14
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TACCACAATATACAGGAGAAATAAGTGAA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-635
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US-09-134-001C-647/c
Sequence 647, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                         27.3%;
66.1%;
LENGTH: 1839 base pairs
                                                                                                                                                                                                                       Query Match 27.3 Best Local Similarity 66.1 Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.1
Best Local Similarity 57.3
Matches 51; Conservative
                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                CDS
331..1602
                                                                  both
                                                                                       MOLECULE TYPE:
                                                                                                                                ; NAME/KEY:
; LOCATION:
PCT-US96-01427-1
                                                                    TOPOLOGY:
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Sequence 693, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
FITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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                                                                                                              Length 810;
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                                                                                                                 DB 4;
                                                                                                           Query Match 27.1%; Score 28.2; D Best Local Similarity 57.3%; Pred. No. 2.8; Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.1%; Score 28.2; D
Best Local Similarity 57.3%; Pred. No. 4.7;
Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DAFE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION UNBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3224 CGCCAGCAGAACCAGGTAAACCAGCGGAA 3252
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APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-A06-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
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                                ORGANISM: Staphylococcus epidermidis
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5510466-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Stap
US-09-134-001C-693
           ; TYPE: DNA
; ORGANISM: Stap
US-09-134-001C-624
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LENGTH: 3552
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5510466-3
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Sequence 624, Application US/09134001C

Sequence 624, Application US/09134001C

Sequence 624, Application US/09134001C

Sequence 624, Application US/09134001C

Sequence 624, Application US-09134001C

TITLE 0F INVENTION: EPEDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPEDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPEDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

NUMBER: US-06-14

NUMBER: US-06-14
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 726
LENGTH: 585
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                                                                                                                                                                                                DB 4;
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                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-647
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-134-001C-726
                                                                                 TYPE: DNA
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Query Match
26.9%; Score 28; DB 6; Length 1588;
Best Local Similarity 58.3%; Pred. No. 4.1;
Matches 49; Conservative 0; Mismatches 35; Indels
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Search completed: February 19, 2003, 22:58:49 Job time: 10.8656 secs

Sequence 4, Appli Sequence 70, App Sequence 72, App Sequence 14, Appli Sequence 14, Appli Sequence 11, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 1293, Ap Sequence 1293, Ap Sequence 1293, Ap Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 27, Appl Sequence 28, Appl Sequence 27, Appl Sequence 28, Appl Sequence 762, Appl Sequence 763, Appl Sequence 764, Appl Sequence 764, Appl Sequence 764, Appl

Sequence:

Run on:

Searched:

Database

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53 GCTGGACCTCCAGCACACCCCAGAGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGT 112
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APPLICANT: Fox, Brian
APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: AZACRE13
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR APPLICATION NUMBER: US 60/253,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 TTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCC 156
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                                Query Match 100.0%; Score 104; DB 9; Best Local Similarity 100.0%; Pred. No. 1.4e-24; Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       US-09-919-497-6
US-09-954-456-762
US-09-764-869-1494
US-09-919-497-7
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US-09-923-876-4300
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1381
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US-09-997-610-5
Sequence 5, Application US/09997610
; Patent No. US20020156244A1
   ORGANISM: Homo sapiens
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Best Local Similarity
NAME/KEY: CDS
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Sequence 58, Appl
Sequence 28, Appl
Sequence 1186, Ap
Sequence 9137, Ap
Sequence 6, Appl
Sequence 6, Appli
Sequence 762, Appli
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                                                                                                                         February 19, 2003, 18:01:21; Search time 8.36875 Seconds (without alignments) 6329.459 Million cell updates/sec
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Sequence 66,
Sequence 53,
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Sequence 69,
Sequence 71,
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                                                                                                                                                                                                                                          1 gctggacctccagcacaccc......agtgaaatgacaaaatgccc 104
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Sequence 3,
Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/DEC_NEM_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-923-779-47
US-09-923-779-66
US-09-923-779-66
US-09-923-779-68
US-09-923-779-69
US-09-923-779-52
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US-09-923-779-52
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US-09-923-779-52
US-09-913-779-52
US-09-913-779-53
US-09-913-779-53
US-09-919-49-66
US-09-954-456-762
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US-09-997-610-5
US-09-997-610-3
US-09-997-610-3
                                                                                                                                                                                                                                                                                                                                   424239 seqs, 254661826 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        nucleic search, using sw model
                                                                                                                                                                                               US-09-997-610-1_COPY_53_156
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                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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                                                                                          OM nucleic -
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Maximum DB
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Gaps

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Result Š Length 1381; Indels ~

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61 TTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1731
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LENGTH: 561
                                                                                                               RESULT 4
US-09-997-610-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3. Application US/09997610
| Patent No. US20020156244a1
| GENERAL INFORMATION:
| APPLICANT: Fox. Brian
| APPLICANT: Holloway, James L.
| TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
| CURRENT FILING DATE: 2001-11-29
| PRIOR APPLICATION NUMBER: US 60/253,924
| PRIOR APPLICATION NUMBER: US 60/253,924
| PRIOR FILING DATE: 2000-11-29
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: FastSEQ for Windows Version 3.0
                  APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRR13
FILE REFERENCE: 00-96
CURRENT PELICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR PAPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.1%; Score 75; DB 9; Length 137 llarity 64.4%; Pred. No. 3.8e-15; Conservative 14; Mismatches 23; Indels
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LOCATION: (1)...(1377)
OTHER INFORMATION: Each n is independently A, T,
NAME/KEY: misc_feature
LOCATION: (1)...(1377)
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; OTHER INFORMATION: n = A,T,C or G
US-09-997-610-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(1731)
US-09-997-610-5
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Matches 67; Conserv
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                              LENGTH: 1731
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US-09-997-610-3
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406 GCNGGNCCNCCNGCNCAYCCNMGNCCNCCNGARGARGARGTNGGNCCNCCNGGNGCNCCNGGN 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Degenerate polynucleotide sequence of zacrp13/zhp1 OTHER INFORMATION: of SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pyle, Ruth A.
APPLICANT: Pyle, Ruth A.
APPLICANT: Yu, Jiangchun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
SURNBER OF SEQ ID NOS: 155
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.1%; Score 75; DB 9; Length 173 Best Local Similarity 64.4%; Pred. No. 4.2e-15; Matches 67; Conservative 14; Mismatches 23; Indels
                                                                                                                                                     Sequence 7, Application US/09997610
Patent No. US20020156244A1
GENERAL INFORMATION:
APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRPI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCC 104
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Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/09923779
Patent No. US20020076721A1
GENERAL INFORMATION:
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LOCATION: 544, 550
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(1731)

CTHER INFORMATION: n = A,T,C or
US-09-997-610-7
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61.6%;
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US-09-923-779-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CTGGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCCTCCTGGTGCACCAGGTT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                       Sequence 51, Application US/09923779; Sequence 51, Application US/09923779; Patent No. US20020076721A1; Sequence 51, Application:
Sequence 1. NeoRANTION:
APPLICANT: PY16, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER;
FILE REFERENCE: 21012.553
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Yu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REPERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SEQ ID NO 66
LENGTH: 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 617;
 Indels
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 33;
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 Mismatches
                                                                                                                                           464 CTCCAGGACCTCCTGGTGCTATAGGT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TACCACAATATACAGGAGAAATAAGT 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
CAGATION: 581, 605
COHER INFORMATION: n = A,T,C or G
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 642, 646
COTHER INFORMATION: n = A,T,C or G
                                                                                                       62 TACCACAATATACAGGAGAAATAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.9%;
Best Local Similarity 61.6%;
Matches 53; Conservative
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                             RESULT 6
US-09-923-779-51
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Matches
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                                                                                                 Gaps
                                                                                                                                                                                    2 CTGGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-923-779-53
Sequence 53, Application US/09923779
Sequence 53, Application US/09923779
Sequence 53, Application US/09923779
Sequence 53, Application US/09923779
Sequence 51, Algory
Sequence 52, Algory
Sequence 52,
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    Length
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Score 33.2; DB 10;
Pred. No. 0.12;
0; Mismatches 33;
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CURRENT FILING DATE: 2001-08-06
NUMBER FILING NOS: 155
SOFTWARE: PASLESQ for Windows Version 4.0
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Patent No. US20020076721A1
GENERAL INFORMATION:
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; LOCATION: 517, 579, 581, 603, 649
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-53
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    31.9%;
61.6%;
Query Match 31.9
Best Local Similarity 61.6
Matches 53; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens US-09-923-779-71
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LENGTH: 780
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GENERAL INCORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Raios, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 2.01.21.553
CURRENT FILING DATE: 2.011-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                            DB 10;
                                                            Query Match 31.9%; Score 33.2; D
Best Local Similarity 61.6%; Pred. No. 0.12
Matches 53; Conservative 0; Mismatches
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Patent No. US20020076721A1
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; LCCATION: 565, 619, 621
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-69
; LOCATION: 654
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-68
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US-09-923-779-71
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LENGTH: 656
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Sequence 5, Application US/09923779;
Fatent No. US20020076721A1
Sequence 5, Application:
APPLICANT: Nu. Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
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     Length 658;
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Sequence 52, Application US/09923779
Sequence 52, Application US/09923779
Sequence 52, Application US/09923779
Sequence 52, Application:
Sequence 52, Application:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
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Best Local Similarity 61.6%; Pred. No. 0.12;
Matches 53; Conservative 0; Mismatches 33;
Score 33.2; DB 10;
Pred. No. 0.12;
                                                    0; Mismatches
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; LCCATION: 627
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-52
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SOFTWARF. PARTY
31.9%; 61.6%;
                                                 Matches 53; Conservative
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     Query Match
Best Local Similarity
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APPLICANT: Tao, Neaghing
APPLICANT: Tao, Neaghing
APPLICANT: Tao, Neaghing
APPLICANT: Tao, Neaghing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLELE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF 1811.201-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1786
LENGTH: 392
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                                                      622, 628, 640, 659, 672, 675, 701,
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GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: W. Jiangchun
APPLICANT: W. Jiangchun
APPLICANT: Walchael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SEQ ID NO 28
LENGTH: 823
                                                                                                                                                                                     Query Match 31.9%; Score 33.2; DB 10; Length 780; Best Local Similarity 61.6%; Pred. No. 0.13; Matches 53; Conservative 0; Mismatches 33; Indels 0;
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; FEATURE:

NAME/KEY: misc_feature

; LOCATION: 456, 489, 532, 562, 608,

LOCATION: 704, 712, 718, 772, 779

; OTHER INFORMATION: n = A,T,C or G

US-09-923-779-5
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; ORGANISM: Homo sapiens
US-09-923-779-28
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US-09-960-352-1786
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US-09-923-779-28
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Human breast cance Coding sequence for Bovine alphal(III) Bovine alphal(III) Porcine alphal(III) Vector pac3Al cont Collagen type III

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cDNA #28 encoding

Human collagen XI CDNA #49 encoding DNA encoding novel Human Tumour Endot

Human Tumour Endot DNA encoding novel

Lung cancer relate Human endometrial Human polynucleoti

Human 1mmune/haema cDNA #4 encoding h Murine HSP47 inter Human 1mmune/haema

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Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Colon adenocarcino

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Human; gene; ss; gene therapy; genset metabolic gene; GMG-78; GMG-8; GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; heart disease; cardiac insufficiency; coronary insufficiency; high blood pressure; insulin sensitiser; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genset metabolic gene (GMG-9) cDNA sequence.
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/note= "No stop codon is given"
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AAS89670
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AAS34830
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AAS79378
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ABK35486
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AAH48067
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ABL51009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL44066 standard; cDNA; 1338 BP.
  15-JAN-2002; 2002WO-IB01215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse ischaemic co
Human EST-derived
Human EST-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA #47 encoding
cDNA #51 encoding
cDNA #66 encoding
cDNA #53 encoding
cDNA #68 encoding
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                                                                                          (without alignments)
6506.903 Million cell updates/sec
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2. \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
4. \SIDS2/gcgdata/geneseqg-embs/NA1981.DAT:*
5. \SIDS2/gcgdata/geneseqg-embs/NA1983.DAT:*
5. \SIDS2/gcgdata/geneseqg-embs/NA1983.DAT:*
6. \SIDS2/gcgdata/geneseqg-embl/NA1984.DAT:*
7. \SIDS2/gcgdata/geneseqg-embs/NA1981.DAT:*
8. \SIDS2/gcgdata/geneseqg-embs/NA1981.DAT:*
8. \SIDS2/gcgdata/geneseqg-embl/NA1981.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA1981.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA1981.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA1991.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA2001A.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA2001A.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA2001A.DAT:*
9. \SIDS2/gcgdata/geneseqg-embl/NA2001A.DAT:*
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                                                                             February 19, 2003, 15:08:07; Search time 35.9937 Seconds
                                                                                                                                                  1 gctggacctccagcacaccc......agtgaaatgacaaatgccc 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
         5.1.3
Compugen Ltd.
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                                                                                                                                                                                                           2185239 seqs, 1125999159 residues
          GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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104
                                                       nucleic search, using sw model
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ABI99819
AAH98343
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Human polynucleoti Human cDNA differe Lung cancer relate Human contig polyn Human EDA1-II exon

Human EDA1-II enco CDNA encoding nove Human EDA1-II open

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02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               AAH98343;
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                                                                                                                                                         The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; and heart diseases (e.g. cardac insulficiency, coronary insufficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present CDNA
                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                     obesity, impaired glucose tolerance, insulin resistance, Syndrome X, Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                          38 TGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ischaemic condition related cDNA sequence SEQ ID NO:932
                                                                                                                                                                                                                                                                                                    Length 1338;
                                                                                                                                                                                                                                                                                          Score 59; DB 24; Length LL. Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishii Y;
                                                                                                                                                                                                                                                                                 Sequence 1338 BP; 359 A; 288 C; 350 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi Y, Nagata T,
                                                  Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                             sequence encodes the human GMG-9 protein.
                                                                                                                                         Disclosure; Page 122-124; 128pp; English.
                                                 Bihain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABI99819 standard; cDNA; 6512 BP
                                                                                                                                                                                                                                                                                                   56.7%;
92.5%;
          16-JAN-2001; 2001US-262235P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                        Conservative
                                                 Bour BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishikawa K, Asai S,
                                                                    WPI; 2002-557821/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-034733/04.
P-PSDB; ABB57334.
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Best Local Similarity
                                                                               P-PSDB; AAO15423
                                                                                                                                                                                                                                                                                                                                                                                                     AATGCCC 116
                                                                                                                                                                                                                                                                                                                                                                                  98 AATGCCC 104
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                             (GEST ) GENSET
                                                 Erickson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
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                                                                                                                                                                                                                                                                                                                        62;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a genes (I) in a test sample condition genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia) or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; ht tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6512 BP; 1553 A; 1798 C; 1950 G; 1211 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.8; DB 24;
Pred. No. 0.065;
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Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TACCACAATATACAGGAGAAATAAGTGACAA
                                                                                                                                                                      Claim 2; Page 2340-2352; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH98343 standard; cDNA; 5467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.4%;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
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P-PSDB; AAM23684.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200154477-A2.
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TCTCCAGGATACCAAGGACCCCCTGGTGAA 720
                                                                                                                                                                                                                                                     TTACCACAATATACAGGAGAAATAAGTGAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 126; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                 ABK44107 standard; cDNA; 561
                                                                                                                           32.7%;
ilarity 61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2000; 2000US-223130P.
30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-2001; 2001WO-US24619
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                                                                                                                                        Local Similarity
nes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200212331-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                             Query Match
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Matches
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                                                                        The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                  1 GCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGAGTGGGGGCCTCCTGGTGCACCAGGT 60
Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide for treatment of diseases, diagnostics, raising and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomatc, monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition; ss.
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                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                     Length 5467;
                                                                                                                                                                                                                    Sequence 5467 BP; 1330 A; 1323 C; 1550 G; 1264 T; 0 other;
                                                                                                                                                                                                                                                                                    0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human EST-derived coding sequence SEQ ID NO: 268.
                                                                                                                                                                                                                                                   Score 34; DB 22;
Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qian XB, Wang Z,
J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                       TCTCCAGGATACCAAGGACCCCCTGGTGAA 720
                                              Claim 1; Page 314-315; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 381-382; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                TTACCACAATATACAGGAGAAATAAGTGAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-063870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang J,
                                                                                                                                                                                                                                                ch 32.7%;
1 Similarity 61.1%;
55; Conservative (
              antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US02687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476164/51.
P-PSDB; AAM23752.
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                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                         the invention.
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03-AUG-2000;
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AAH98411 RESULT

Matches

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Cao Y,

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The present invention relates to the isolation of CDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the protein may be used in the diagnosis. Composition and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the partication of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probess or primers for nucleic acid hybridisation assays. ABK44061-ABK4209
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urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour protein; immune response; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGACCTCCAGCACACCCCCAGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                               Length 5468;
                                                                                                                                                                                                                                                                                       Sequence 5468 BP; 1330 A; 1323 C; 1551 G; 1264 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA #47 encoding human pancreatic tumour protein.
                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 22;
Pred. No. 0.5;
0; Mismatches 35;
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Length 617;

DB 24;

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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                          ABK44126;
      Query Match
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                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                 ABK44126
                                                                                                                                                              δ
                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of CDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the protein may be used in the diagnosis. C prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the cevelopment of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probess or primers for nucleic acid hybridisation assays. ABK44061-ABK44209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
represent CDNA sequences encoding for human pancreatic tumour proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent cDNA sequences encoding for human pancreatic tumour proteins
                                                                                                                                                                                      404 CIGGATCICCAGGATACCAAGGACCCCTGGTGAACCTGGCAAGCTGGTCCTTCAGGCC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic; gene; ss.
                                                                                                                     Gaps
                                                                                                                                                            2 CTGGACCTCCAGCACCCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTT 61
                                                                                                                     ;
                                                                                561;
                                                                         Match 31.9%; Score 33.2; DB 24; Length Local Similarity 61.6%; Pred. No. 0.42; les 53; Conservative 0; Mismatches 33; Indels
                                                                                                                   33; Indels
                                       Sequence 561 BP; 121 A; 171 C; 141 G; 126 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA #51 encoding human pancreatic tumour protein.
                                                                                                                                                                                                                                                                             464 CTCCAGGACCTCCTGGTGCTATAGGT 489
                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 127; 167pp; English.
                                                                                                                                                                                                                                        62 TACCACATATACAGGAGAAATAAGT
                                                                                                                                                                                                                                                                                                                                                                               ABK44111 standard; cDNA; 617 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001; 2001WO-US24619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2000; 2000US-223130P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001US-265447P
15-MAY-2001; 2001US-291201P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyle RA, Xu J, Kalos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200212331-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                    ABK44111;
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                          RESULT 6
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Sequence 617 BP; 134 A; 186 C; 157 G; 138 T; 2 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or primers for nucleic acid hybridisation assays. ABK44061-ABK44209 represent cDNA sequences encoding for human pancreatic tumour proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development of cancer in a patient, or as markers for the progression
of cancer. The polynucleotide sequences may also be used as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pancreatic tumour protein; immune response; pancreatic cancer;
                                                                                                                                                                                  Gaps
                                                                            Gaps
                                                                                                                                          2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development of cancer; cancer progression; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA #66 encoding human pancreatic tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.9%; Score 33.2; DB 24;
Best Local Similarity 61.6%; Pred. No. 0.44;
Matches 53; Conservative 0; Mismatches 33;
Score 33.2; DB Pred. No. 0.43; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 132; 167pp; English.
                                                                                                                                                                                                                                                                                     62 TACCACAATATACAGGAGAAATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK44126 standard; cDNA; 648 BP
       31.9%;
61.6%;
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30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-2001; 2001WO-US24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyle RA, Xu J, Kalos MD;
                                                                        53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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pancreatic tumour protein; immune response; pancreatic cancer; pment of cancer; cancer progression; cytostatic; gene; ss.

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cDNA #68 encoding human pancreatic tumour protein.
                          62 TACCACAATATACAGGAGAAATAAGT 87
                                                                                                                                        ABK44128 standard; cDNA; 655
                                                                                                                                                                                                                   21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                        development of
                                                                                                                                                                             ABK44128;
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                      Novel polynuclectide encoding pancreatic tumour polypeptides, useful pharmaceutical compositions, e.g. vaccines, for treating pancreatic
2 CTGGACCTCCAGCACACCCCAGGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 653 BP; 153 A; 188 C; 167 G; 140 T; 5 other;
                                                                                                                                                                                                                                                                                                                                     cDNA #53 encoding human pancreatic tumour protein.
                                                                                                   464 CTCCAGGACCTCCTGGTGCTTAGGT 489
                                                                          62 TACCACAATATACAGGAGAAATAAGT 87
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                                                                                                                                                                                                                     ВЪ.
                                                                                                                                                                                                                 ABK44113 standard; cDNA; 653
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30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic `
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent cDNA sequences encoding for human pancreatic tumour proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of cDNA sequences
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Pred. No. 0.44;
0; Mismatches 33; Indels 0.
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30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                    06-AUG-2001; 2001WO-US24619.
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Best Local Similarity 61.6
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu J, Kalos
                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-241741/29.
                                                            WO200212331-A2.
Homo sapiens.
                                                                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyle RA,
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DB 24; Length 653;

31.9%; Score 33.2; DB 24; Length llarity 61.6%; Pred. No. 0.44; Conservative 0; Mismatches 33; Indels

Similarity

Local Best Loca Matches

Query Match

53;

CTGGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 61

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(first entry)
                                                                                                                     Homo sapiens.
                                21-MAY-2002
                                                                                                                                                                   14-FEB-2002
           ABK44131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK44112;
                                                                                                                                                                                                                                                                                        Pyle RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of CDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the protein may be used in the diagnosis. C prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the compositions cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays. ABK44061-ABK44009
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                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent cDNA sequences encoding for human pancreatic tumour proteins.
                                                                                                                               Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 656 BP; 152 A; 188 C; 168 G; 145 T; 3 other;
                                                                                                       cDNA #69 encoding human pancreatic tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.2; DB Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 CTCCAGGACCTCCTGGTGCTATAGGT 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 133; 167pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK44131 standard; cDNA; 658 BP.
                               ABK44129 standard; cDNA; 656 BP
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61.6%;
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                                                                                                                                                                                                                                                                          30-JAN-2001; 2001US-265447P.
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                                                                               21-MAY-2002 (first entry)
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Best Local Similarity
                                                                                                                                                                                         WO200212331-A2
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                14-FEB-2002.
                                                        ABK44129;
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       RESULT 10
ABK44129
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The present invention relates to the isolation of CDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the presence of cancer in a patient. A composition comprising the polynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosis. Prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the cancer of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays. ABK44061_ABK4209
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                                                                                    Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic; gene; ss.
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cDNA #71 encoding human pancreatic tumour protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 133; 167pp; English.
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30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
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The present invention relates to the isolation of CDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the protein may be used in the diagnosis, or prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the compositions of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays. ABK44061-ABK44209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or primers for nucleic acid hybridisation assays. ABK44061-AbK44209 represent cDNA sequences encoding for human pancreatic tumour proteins
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   development of cancer; cancer progression; cytostatic; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.47;
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61.6%;
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                                                                                                                                                                                                                                                                                                                              2000US-223130P.
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Best Local Similarity
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                                                                                                                                 WO200212331-A2
                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                           07-AUG-2000;
30-JAN-2001;
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                                                                                            Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic; gene; ss.
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1.ve 0; Mismatches 33; Indels 0;
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                             cDNA #52 encoding human pancreatic tumour protein.
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30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
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Conservative
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                                                                                                                                                                                                Homo sapiens.
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NAME OF THE PROOF 
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Search completed: February 19, 2003, 22:56:18
Job time : 40.9937 secs
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                                                                                                                                                                                                                                                                                                                                             encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for sequences encoding human pancreatic tumour proteins are useful for cancer in a patient that expresses these polynucleotides is useful for determining the presence of cancer in a patient. A composition comprising the prolynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosis. Prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the converted of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probess or primers for nucleic acid hybridisation assays. ABK44061-ABK44209
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0
                                                                                                                                                                                                                                           Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent cDNA sequences encoding for human pancreatic tumour proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cancer related protein coding sequence SEQ ID NO: 58
                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; DB 24; Length 823; 0.48;
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Pred. No. 0.48;
0; Mismatches
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                                                                                                                                                                                                                                                                                                   Claim 1; Page 119; 167pp; English.
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1 Similarity 61.6%;
53; Conservative
                                                                                       07-AUG-2000; 2000US-223130P.
30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-2000; 2000WO-US17536.
                                                           06-AUG-2001; 2001WO-US24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001 (first entry)
                                                                                                                                                                                 Pyle RA, Xu J, Kalos MD;
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                                                                                                                                                    (CORI-) CORIXA CORP
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Best Local Similarity
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WO200212331-A2
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AAF44902
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                                                                                                                                                                                                                                                                           New polynucleotides encoding breast tumor specific proteins, useful for prevention, treatment and diagnosis of breast cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGAGTGGGGCCTCCTGGTGCACCAGGTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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99US-0140903.
99US-0158980.
                                                                                                                                                       Mitcham JL;
                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                              WPI; 2001-041426/05.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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February 19, 2003, 23:16:26; Search time 331.581 Seconds (without alignments) 9128.055 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

1 gctggacctccagcacaccc.....agtgaaatgacaaatgccc 104 US-09-997-610-1\_COPY\_53\_156 104 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb\_ro:\* gb\_sts:\* em\_ro:\* em\_sts:\* gb\_vi:\* em\_ba:\* em\_fun:\* em\_hum:\* gb\_sy:\* gb\_ba:\*
gb\_ntg:\*
gb\_on:\*
gb\_on:\*
gb\_ov:\*
gb\_ph:\*
gb\_pl:\* em\_pat:\* em\_in:\* еш\_mu:**\*** em\_om:\* em\_or:\* еш\_оv:\* em\_ph: em\_pl:\* GenEmbl: \* Database :

em\_htgo\_hum:\*
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em\_htg\_other:\* em\_htg\_mus:\* em\_vi:\* em\_htg\_hum:\* em\_htg\_inv:\*

em\_un:\*

em\_htg\_pln:\* em\_htg\_rod:\* em\_htg\_mam:\* Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	282198 Human DNA s AF282902 Hydra vul AJ420010 Ostertagi X06777 Mouse mRNA AX306181 Sequence	<b>∑</b> ≻ Ø		U57362 Rattus norv AC010289 Homo sapi AC084840 Homo sapi AC08615 Homo sapi AC08615 Homo sapi AC098586 Homo sapi AC098869 Homo sapi AC093809 Homo sapi AC093809 Homo sapi AC083802 Homo sapi AC084810 Homo sapi AC07354 Sequence BC028178 Homo sapi AX1667354 Sequence	AX146424 Sequence AX302553 Sequence AX302553 Sequence AX302553 Sequence E10600 cDNA encod1 X14420 Human mRNA AC022708 Homo sap1 AC084440 Caenorhab AC02249 Homo sap1 U84501 Caenorhab U82327 Caenorhabd1
SUMMAI	EKO K	MUSCOL HSNCOL1 CEF57B1 CEY51H4 AE01055			AX146424 AX146430 AX302553 AX393295 E10600 HSCOL3A1 AC022708 AC022708 AC022249 CB04440 AC022249 CB04479 CBU22327
Length DB	7.145880 0 5851 0 287 4 3612 4 6512	6512 8 694 8 36532 8 269619 2 11942	5 3734 5 6522 9 31110 7 3234	107083 9 107083 9 1107083 9 1167416 9 1155600 2 1167214 9 1167214 9 116884 9 118884 0 118881 6 9 1881 6 9 3902 6	99 4428 4428 90 90 90 90 90 90 90 90 90 90
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ALIGNMENTS

HS302D9 1458B0 bp DNA linear PRI 12-DEC-1999 Human DNA sequence from clone RPI-302D9 on chromosome 22 Contains Homo sapiens.

Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 145880)

Bridgeman, A.

Direct Submission GSSs, complete sequence. 282198 282198.2 GI:6572207 HTG. RESULT 1 HS302D9 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

matches matches matches matches tches 25 atches 1 atches 1 atches 1 atches 3 matches 0678) m:AQ7014 m:AQ7014 m:AQ254	misc_feature   /note="match: GSS: Em:B14024"	7.7
COMMENT  CBLO 15A, UK. E-mail enquiries: hunquery Bsanger.ac.uk Clone  CBLO 15A, UK. E-mail enquiries: hunquery Bsanger.ac.uk Clone  CBLO 15A, UK. E-mail enquiries: hunquery Bsanger.ac.uk Clone  requests: clonerquest Gespanger.ac.uk  On Dec 13, 1999 this sequence version replaced gi:3164067.  During sequence assembly data is compared from overlapping clones.  Where differences are found these are annotated as variations stored that the note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, we submit sequences with corresponding to the overlapping clone, as submit sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Meret the aspectance is ambiguous, there is an annotation using the 'unsure' feature key.  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  Em: EMBL: Sw., SWISSEROT; TT: TERMEL, Mp: WORMPEP information on the WORMPEP database can be found at the primary accession checking from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22, constructed by the Sanger Centre Chromosome 22, constructed by the group of Pieter de Jong. For further detabls see http://www.sanger.ac.uk/PIG/CDL2 as Found at the Roswell RP1-302D9 is from the library RPCI-1 constructed at the Roswell RP2-302D9 is from the library RPCI-1 constructed at the Roswell RP2-302D9 is from the library RPCI-1 in the library RPCI-1 clone RP1-302D9 The true left end of clone CTA-28PF2 is at 65682 in this sequence. The true right	onsensus" sensus" sensus" sensus" consensus" sensus" consensus" sensus" consensus" sensus" consensus" sensus"	.2705 of consensus"

us-09-997-610-1\_copy\_53\_156.rge

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Fowler, S.J. and Boot-Handford, R.P.
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      AUTHORS
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    (bases 1 to 5851)
    Fowler, S. J., Jose, S., Zhang, X., Deutzmann, R., Sarras, M.P. Jr. and
Boot-Handford, R.P.

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Hydridae; Hydra.
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Hydra vulgaris type IV collagen alpha 1 chain precursor, mRNA,
complete cds.
                                                                                                                                                                                           /note="MSTA repeat: matches 2. .29 of consensus"
18324. .18392
/note="MER66-internal repeat: matches 4919. .4993 of
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/note="AluSc repeat: matches 1. .299 of consensus"
16028. .16245
/note="MLT1B repeat: matches 178. .390 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER66-internal repeat: matches 4548. .4919 of
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/note="MER66-internal repeat: matches 2186. .2417 of the consensus" Andrew Consensus Consen
                                                                                                                                                                                                                                                                                                                                   /note="AluJb repeat: matches 1. .311 of consensus" 18713. .19133
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/note="MER66-internal repeat: matches 1210. .2186
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23905. .23989
/note="MER66-internal repeat: matches 3017. .3102
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J. Biol. Chem. 275 (50), 39589-39599 (2000)
20564332
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2 (bases 1 to 5851)
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/note="match: GSS: Em:AQ005063"
19251. .19719
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19537, .20290
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18393. .18712
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/note="AluSp :
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Hydra vulgaris
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SOURCE
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AF282902
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IGPQGPQGDKGDQGQSVIGPKGETGAIGKKGETGQDGLKGRDGIGKQGANGEKGEKGN
SVVGLPGDPGEKGSPGEKGKDGISGKQGKPGPPGKDGVDGTPGKDGLPGNPGPEGPKG
EKGVTGPTGLDGEKGEPGSSGQKGAKGETGVRGKPGATSNVMGPKGNRGESGAKGEPG
                                                                                                                                                                                                                                            /codon_start=1
/product="type IV collagen alpha 1 chain precursor"
/protein_id="AAG40729.1"
/db_xref="GI:l1875612"
/translation="MNHTTKWTIWIVLIFTLHSCLVFTQLCGGGGCNQCSNVCVGQKG
                                                                                                                                                                                                                                                                                                                                                                                                DRGSVGLPGFKGPIGEPGFPGGEGPAGRPGEKGDGGAPGLQGEVGARGKVGPPGTPGI
PGSHGRPGDEGRQGEPGLPGCNGTKGDIGPPGPRGKDGVQGPSGLPGPIGPPGEPGDS
TATKLKGQKGEPGPKSQDGPAGDPGTKGDKGESGKAGRMGPQGLRGEKGARGDSNITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGERGDKĞDIGLPGPPGRDCNGSSVTGELITNIQGPKGEQGKKGDQGQKGEPGQPGQA
GEAGQDGQKGEKGDKGEIGSAGPSGIQGEKGDIGATGAAGTKGEPGSDGSLGSPGQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHGTKGSEGPVGDRGKQGESITGPPGJIGEKGQRGPEGKKGEPGPEGPPGPNGEVGDT
GPPGLKGLKGEIGMTGPSGEPGKTGAEGMKGPIGPAGQRGETGSKGESGRPGQSVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQGPPGABGPQGEKGERGIGTDKGTKGDTGDIGLQGPKGERGERGERGEGGRKGDQGPIGP
KGDVGEPGPAGSIGNTGISGNDGPKGESGPPGIKGEPGSVGSIGPKGSKGEQGEKGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSTLKGNPGPEGPRGPTGPPGPAGKDYILDLEVGPLGEKPTKGEPGEDGPKGDKGDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETGSQGTKGEKGVPGSKGEKGEQGLEGPKGLEGRVGLAGSKGDKGIKGVIGKPGPTGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRGEKGEAGORGYKGEPGPSSOLTINPGAKGEOGDRGIKGEKGNIGPKGINGPFCKDG
SIGPEGPKGDSGOKGETGLDGPKGEKGOPAIGTGPKGEKGDQGPPGPPGPQGDIGEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSTMPFLECDIQNKCVVASRNDYSFWLSTAEKPKEAPSSGADLENYISRCIVCEAPSH
VLAVHSQSELDPKCPDGWENLWTGFSFLMYNSAGAQGSGQLLSSSGSCLEDFRVNPYI
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                                     Sciences, University
PT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECHGRGTCWYYGPTLSFWLSTIGESNMFQVPKFEILERNLKARVSRCAVCMKSVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Region: contains collagenous domain"
Direct Submission
Submitted (27-JUN-2000) School of Biological Sci
of Manchester, Oxford Road, Manchester M13 9PT,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
4642. .5325
/note="Region: non-collagenous domain"
1 942 c 1638 g 1318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Region: non-collagenous domain"
277. 4641
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                                                                                                                                                /organism="Hydra vulgaris"
/db_xref="taxon:6087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="N-glycosylation'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 61; Conserv
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DEFINITION
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OMGSSFQGPKGDKGEQGVSGPPGVPGQAQVKEKGDFAPTGEKGQKGEPGFPGVPGYGE
KEPPGKQFGPKGKPGKDFGKBRGSPGT FGDSGYPGLPGRQFGPSGEKGEALPGPPGTY
TGTMPLAGEKGDRGY FCAPGLINGEPGPKGFPGTPGLACPPGFPPTPGQAQAAPGFPGENGE
KGDQGFPGVSFPGFSGRDGAPGPPGPPGPPGGPGTHVGIVECQPGPPGGPPGGPPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGLTGEVGOKGOKGESCLACITEGLRGPPGLGCPPGEIGFPGHPGAKGDRGLPCRDGL
EGLPCPQGSPGLIGQPGAKGEPGEIFFDMRLKGDKGDPGFPGQPGMPGRAGTPGRDGH
PGLPGPKGSPGSIGLKGERGPPGGVGFPGSRGDIGPPGPPGVGPIGPVGEKGQAGFPG
shows interrupted GlyXY nature of collagen alpha chain. Data kindly reviewed (02-SEP-1988) by Wood L. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:P02463"
/translation="MGPRLSVWLLLFAALLLHEERSRAPAKGDCGGSGCGKCDCHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGGKGERGLPGLQGVIGFPGMQGPEGPHGPPGQKGDAGEPGLPGTKGTRGPPGAAGYP
GNPGLPGIPGQDGPPGPPGIPGCNGTKGERGPLGPPGLPGFSGNPGPPGLPGMKGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPGSPGLPGPKGEAGKVVPLPGPPGAAGLPGSPGFPGPOGDRGFPGTPGRPGIPGEKG
AVQPGPGIPFPCLPGPKGVDGLPGEIGRPGIPGRPGFWGLPGPGQOKGEPGIGLPG
LKGCPGLPGTPGTPFEKGSIGGPGPGEEGGITGPPGLQGIRGDPGPPGVGARPPPG
FGIGPPGAMGPPGGQGPPGSSGPPGIKGEKGFPGFPGLDMPGPKGDKGSOGLPGLTGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGLPGLPGQQGTPGVPGFPGSKGEMGVMGTPGQPGSPGPAGTPGLPGEKGDHGLPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPRGDPGFKGDKGDVGLPGMPGSMEHVDMGSMKGQKGDQGEKGQIGPTGDKGSRGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGSQGVPGSPGEKGAKGEKGQSGLPGTGTPGRPGDKGDQGLAGFPGSPGEKGEKGSAG
TPGMPGSPGPRGSPGNTGHPGSPGLPGEKGDKGLPGLDGVPGVKGEAGLPGTPGPTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EILGHVPGTLLKGERGFPGIPGMPGLPGLPGLQGPVGPPGFTGPPGPPGPPGEKG
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                                                                                                                                                                                                                                                                                                                                /note="collagen alpha chain precursor (AA -27 to 1127)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2711 CAGGACAGTCAGGCCTTCCTGGACAGCAGGGGACACCTGGAGTTCCAGGGT 2770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       883. 3612
/note="helical region (AA 218-1127)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="N-telopeptide (AA 1-15)"
                                                                                                      /db_xref="taxon:10090"
/clone="pcIV-1-PE12, pcIV-1-PE16"
/clone_lib="PYS cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36.8; DB 10;
Pred. No. 0.59;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151. .231
232. .882
product="7S protein (AA 1-217)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="NC2 domain (AA 218-230)" 3475. .3555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 97
                                                                                                                                                                                                                                                               /note="c was deleted [1]"
                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA29946.1"
/db_xref="GI:50502"
                                                                1. .3612
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="MGD:MGI:88454"
                                                                                                                                                                          75. .76
/note="uc was cc in [1]"
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3475, .3555
/note="exon 4 region"
...1 c 1212 g
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/citation=[1]
                                                                                                                                                                                                                                                                                 /citation=[1]
151. .>3612
                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                /citation=[1]
131
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1 Similarity 61.5%;
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGOKGEPG
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Best Local Similarity
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mat_peptide
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                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 10-FEB-1999
                                                                                                                                                                       De Maere, V., Vercauteren, I., Claerebout, E. and Vercruysse, J. Identification of potential protective antigens with local antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertaglinae; Ostertagia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library). See M12879 for genomic exon 14 sequence with differences. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         Submitted (13 NOV-2001) De Maere V., Parasitology, University of Ghent, Salisburylaan 133, 9820 Merelbeke, BELGIUM Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     אסא באיי אווא א 10-FEB-1 Mouse mRNA for basement membrane (type IV) collagen alpha chain.
X06777
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See M1402 for overlapping sequence (cDNA clone pCIV-1-225, same
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/organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
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Pred. No. 0.28;
2; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="collagen"
/protein_id="CAD12264.1"
/db_xref="GI:17065951"
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/gene="col"
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col gene; collagen.
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Ostertagia ostertagi
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2 (bases 1 to 287)
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GNPGLPG1PGQDGPPGPPG1PGCNGTKGERGPLGPPGLPGFSCNPGPPGLPGMKGDPG
EILGHVPGTLLKGERGFPG1PGMPGSPGLPCLQGPVGPPGFTGPPGPPGPPGPPGEKG
                    PAT 11-DEC-2001
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus 13.5 day old embryo parietal endodoerm cDNA to mRNA.
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Muthukumaran,G., Blumberg,B. and Kurkinen,M.
The Complete primary structure for the alpha 1-chain of mou collagen IV. Differential evolution of collagen IV domains
J. Biol. Chem. 264 (11), 6310-6317 (1989)
2703490
On Oct 8, 1994 this sequence version replaced gi:340547.
                                                                                                                                                                                            ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y. Method for examining ischemic conditions Patent: Wo 0188188-A 932 22-NOV-2001; School Juridical Person Nihon University (JP) Location/Qualifiers
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/protein_id="AAA50292.1"
/db_xref="GI:556297"
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/tissue_type="parietal endodoerm"
/dev_stage="13.5 day old embryo"
1. .6512
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Sequence 932 from Patent WO0188188.
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/organism="Mus musculus"
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132. .5141
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/gene="Col4a-1"
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AX306181.1 GI:17645461
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TKGQPGLPGTPGFRKGSTGGRCPVBCBGGLTGPPGLLQGTRCPPGPVGGPRGPPGV
PGGQPCLPGTPGFRKGSTGGPCVPGPCBGGLTGPPGLLQGTRCPPGTAGGTPGPGAWGPPGLPGC
PGGPPGAWCPPGCPPGSSGPPGTKGEKGPPGFPGLLMPGPKGDKGSQGLPGLTG
SGLPGLPGPGAPGCPPGVPGFPGSKGEMGVWGTPGQPGSPGPAGTPGLPGEKGDHGLPGSS
GPRODPGFRCAGNGLDGMCSMEHVPMGSWKGQKDQGERGQIGPGTPGSGPGPG
TPGVPGKCDGQAGHPGQPGKNGPPGLSGTPGSPGLPGPKGSVGGWGLPGSPGSKGPPG
PGSQGVPGSPGEKGAKGEKGQSGLPGIGIPGRPCGDKGDQGLAGFPGSPGEKGSKGSAG
                                            EGLPGPQGSPGLIGQPGAKGEPGEIFFDMRLKGDKGDPGFPGQPGMPGRAGTPGRDGH
PGLPGPKGSPGSIGLKGERGPPGGVGFPGSRGDIGPPGPPGVGPIGPVGEKGQAGFPG
GPGSPGLPGPKGEAGKVVPLPGPPGAAGLPGSPGFPGPQGDRGFPGTPGRPGIPGEKG
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AGQKGEPGSDGIPGSAGEKGEQGVPGRGFPGFPGSKGDKGSKGEVGFPGLAGSPGIPG
VKGEQGFMGPPGFQGDPGLPGTPGHPVEGPKGDRGPQGQPGLPGHPGPMGPPGFPGIN
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PGTPSVDHGFLVTRHSQTTDDPLCPPGTK1LYHGYSLLYVQGNERAHGQDLGTAGSCL
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APAMVMAVHSQTIQIPQCPNGWSSLWIGYSFVMHTSAGAEGSGQALASPGSCLEEFRS
APFIECHGRGTCNYYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMRR
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KGDOGFPGVSLPGPSGRDGAPGPPGPPGOPGHTNGIVECOPGPPGDOGPPGTPGO
                    PGLTGEVGOKGESCLACDTEGLRGPPGPGCPPGEIGFPGQPGAKGDRGLPGRDGL
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X61045 S6747
Callagen homologue; N-COL 1 gene; nematocyst.
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/gene="Col4a-1"
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5777. .5782
/gene="Col4a-1"
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/gene="Col4a-1"
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/gene="Col4a-1"
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Matches 59; Conserv
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                Kurz,E.M.
Direct Submission
Submitted (22-JUL-1991) E.M. Kurz, University of Munich, Dept of
Zoology, Luisenstr 14, Munich 2, GERMANY
                          Eŭkaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
1 (bases 1 to 694)
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                                                                                                                                         Kurz, E.M., Holstein, T.W., Petri, B.M., Engel, J. and David, C.N.
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Pred. No. 0.74;
0; Mismatches 33; Indels (
                                                                                                                                                                                                                                                   /organism="Hydra sp."
/strain="sF1"
/db_xref="taxon:6086"
/clone="3, 2/55"
/clone_lib="lambda gt10, I-cellspec."
                                                                                                                                                      Mini-collagens in hydra nematocytes
J. Cell Biol. 115 (4), 1159-1169 (1991)
92064646
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197 c 123 g 156 t
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/db_xref="G1:9447"
/db_xref="SPTREMBL:Q00484"
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/product="mini-collagen"
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Location/Qualifiers
1. .694
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/gene="N-COL 1"
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62.9%;
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Current sequence finishing criteria for the C. elegans genome sequenced finishing criteria for the C. elegans genome sequenced consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone F57B1. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F57B1 is at 1 in this sequence. The true right end of clone F57B1 is at 1 in this sequence. The true right end of clone F57B1 is at 2573 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTISNIRAEFSAHDKQLDFKTDHLEKILLENVIEHSKWKESAIEELKQIKLMOAEISD
ALQQMKKEIDDAKSTKIIHSTPEKAPETAPTASLPPSSQLQPMHITRRALLGVNVANS
LIGASIDHSCSSRPYSAKDGFFYDFMSYFGTFQBGYALLDRDVLSPGEAWCTYDKRAT
LICKLARFYDFSSYQHYMSGIVPNHAPKLYDVVACTDSCCTKWQPLVANCEYKER
DGSYDBQQFCSVPPTQNHSFINHVQFRFRENHGDMPKTCAYLIRVYGEPVDPKEFT
PWTDNGTESKLESAIVNSVSETA"
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Location/Qualifiers
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PGTITGTIQRFHESADDSEIDLNSSKFIYKEHFSYKETTSMKKEMWYDWLEYRIRMVR
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                                                                                                                                                                                                                                                                                                                Sims, M.A.

Direct Submission

Submission

Submitted (199-AUG-1996) Nematode Sequencing Project, Sanger

Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:

Jessesanger.ac.uk or rwienmatode wustl.edu

Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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4921. .5024,5071. .5452))
/gene="F57B1.2"
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4921. .5024,5071. .5452))
/gene="F57B1.2"
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Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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CDNA EST yk66999.3 comes from this
CDNA EST yk66999.5 comes from this
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/db_xref="G1:3877753"
/db_xref="SPTREMBL:Q20924"
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/chromosome="V"
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20538. 20687)
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/gene="F5781.4"
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complement(join(10251. .10976,11025. .11240))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNGNAGAPGAPGQVVDVPGTPGPAGPPGPPGPAGAPGQPGOSGSGGPGGPGGPGGDAGA
PGAPGQPGQAGAPGQDGDSGSEGACDHCPPPRTAPGY"
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GADAAVGGFGGSAGGSCCSCGTGAAGPAGSPGQDGAPGNDGAPGAPGNDGAPGNDGAPGNDGAPGNDGAPGNDGAPGNDGAPGNDGAPGNDGAPGNDGAPGSPGOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPDSFCFDCPAGPPGPSGAPGQKGPSGAPGVPGQTGGASLPGPPGPAGPPGPSGQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"predicted using Genefinder
Contains similarity to Pfam domain: PF01391 (Collagen
triple helix repeat (20 copies), Score-44.2,
E-value-9, 7-10, N-3; PF01484 (Nematode cuticle collagen
N-terminal domain), Score-40.6, E-value-1.1e-08, N-1
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complement(join(5920. .6069,6126. .6209,6280. .6408,
                                                                                                                                                                                                                                                                                                                                                                     complement join (10251. .10976,11025. .11240))
/gene="F5781.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA EST Yk33c11.3 comes from this gene CDNA EST Yk70b10.3 comes from this gene CDNA EST Yk70b10.3 comes from this gene CDNA EST Yk10b10.3 comes from this gene CDNA EST Yk10c6.3 comes from this gene CDNA EST Yk100f2.5 comes from this gene CDNA EST Yk99e7.3 comes from this gene CDNA EST Yk72e11.3 comes from this gene CDNA EST Yk72e11.3 comes from this gene CDNA EST Yk70b10.5 comes from this gene CDNA EST Yk10c6.5 comes from this gene CDNA EST Yk10f7.5 comes from this gene CDNA EST Yk279e6.3 comes from this gene CDNA EST Yk279e6.5 comes from this gene
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PASIGOSTHILTILIIWIFSAFWAWNETYNNVSNLFISEWGGGGEFEIEVELOHF"
join (23062 . 23112, 24099 . 24151, 24322 . 24499, 24547 . 24696, 24748 . 24830, 25045 . 25267)
/gene="F57811.6"
/note="Predicted using Genefinder
/note="Predicted using Genefinder
CDNR EST EMBL:T01341 comes from this gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WTMNYCGINLKLNYVIDAVQCKLORSFSAVTLHLCETRLGDSRL
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FICADNANDIAGYAAFATPAQFQLASAWYYSRLRALVYISVIOSLLNGIIVSFLYLG
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SMSSSPSKDDESGDEDSDGLNSNSIIDVITDYPIFCLSRAFVLSNYPRFHPPLHLTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(34555. .34692,34753. .35192,35241.
/gene="F5781.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269619 bp DNA linear INV Caenorhabditis elegans cosmid Y51H4A, complete sequence. AL132952 AL031B23 AL031B23 HTG.
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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/note="predicted using Genefinder"
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Pred. No. 1.2;
0; Mismatches
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Caenorhabditis elegans
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Matches 53; Conserv
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EVGPOSNCFSTRSPOTTOKVLWSFRCTDSPLQLTDETLDFFTGKKOFFPDAGNIFTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKDATREMSDHDKLMKYRTVQWCDNTSLKYSRRQILHSNALRIFIDSAVGSNAILSKL
LFEDVKNTTIKKQKHNFKQRKKYRTFENVFEKFREKTLNLELFFRCFNTCIFRSNRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNSAANLNFATILVFFLIFWQFFDFLEASKCTDCIASGKHWCVTVNECGFSPCATSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(50748. .50898,51588. .51977,52741. .52920,53245. .53366,53557. .53611,54196. .54274,54700. .54854,55009. .55055,57258. .57575))
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                                                                                                      AKTKDGIREVFEKATQAALQQKKKKKSKCMIL"
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CDNA EST yk340d3.3 comes fr
CDNA EST yk2991.3 comes fr
CDNA EST yk4991.5 comes fr
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CDNA EST yk47991.5 comes fr
CDNA EST yk486f5.5 comes fr
CDNA EST yk573a7.3 comes fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone Y51H4A. The true left end of clone Y43D4A is at 193825 in this sequence. The start of this sequence (1.115) overlaps with the end of sequence AL713992.

The end of this sequence (269514. .269619) overlaps with the start of sequence AL132846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAENSKNLEKSSOSNDPENAEETEMVIELHTEAAPVENYLEEEIQIKVPEVEEDTEKT
PAGSBKRSTSSCISSELLSEGSIGTCALVEFTNFTLYGFRHTAEPVCCRVLARFOFO
PROCEKFSSISPRESSFPLDPATSSYSAPLSNFTERFRIPINYPRMMSEEFESLHKCIEK
RKSDIRDLLRRIQSAKRRHRRFSEHLQQVQHDHHIDY
Comptement (join (12157. .12228, 13962. .14312, 16459. .16593, 17111. .77131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLLVLVLLIFTILLEFYFGKLLIFGKQKIVENSIEKINSNGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(12157. .12228,13962. .14312,16459. .16593,
17111. .17131))
/gene="Y51H4A.3"
                                                                                                                         Submitted (27-001-1999) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On May 14, 2001 this sequence version replaced gi:5730145.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                    Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/acc/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family), Score=317.2, E-value=6.4e-92, N=1
CDNA EST yk60d10.5 comes from this gene
CDNA EST yk77f3.5 comes from this gene
CDNA EST yk77f3.5 comes from this gene
CDNA EST yk77f3.5 comes from this gene
CDNA EST yk73f3.75 comes from this gene
CDNA EST yk73f3.75 comes from this gene
CDNA EST yk73f3.75 comes from this gene
CDNA EST yk73f3f7.5 comes from this gene
CDNA EST yk73f3f2.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(2293. .2346,2393. .2610,2668. .2758, 3398. .3694,5250. .5357))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(2293. .2346,2393. .2610,2668. .2758,
3398. .3694,5250. .5357))
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comes from this gene
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1. .269619
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                           The C.elegans Sequencing Consortium. 2 (bases 1 to 269619) Sulston, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:09NAE5"
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yk651f5.5 c
yk671f3.5 c
yk5761f3.5 c
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                                                                                                                                                                                                                                                                                                                 available information.
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CDNA EST
                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          name=Y51H4A
IMPORTANT:
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                                              REFERENCE
AUTHORS
TITLE
PUBMED
REMARK
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                                                                                                                            JOURNAL
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nucleatum subsp. nucleatum ATCC

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GDIKNSRVARSNKKALTRLGAKVTFVPPEIWKDESLGEFVNFDDVIDKVDICMLLRVQ
HERHTDSKERREFSRDYKKSFGLTEBRYKRLKEGATIMHPAPVNRDVEIADSLVESE
KSRIFEQMRNGMFMRQAILEYIIEKNKL"
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MLMGAELLINK ATVAH CEDNSLIRGGAMHEGKESAELGIKGIPSICES TO ESTOIVROVILAEA

ANCHYHVCHISAKES VRAVERGKK NOIK VTCEVT PHHILLS ODEDIKEDGMWK MNPPL

KREBENNALIT VGILDGTIDITAT DIAT DIATAHT PHEREKIRGIES SEGIUGSET AF AOLYTKE

KRUDIF SLEMLVKLASENVARIEDRY TO LENDEN TERNORMEN SEGIUGSET AF SOLT K

KRIDIF SLEMLVKLASENVARIEDRY TO LENDEN TERNORMEN SEGIUGSET AF SOLT TO THE SEGIOUS SEGIO
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Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,
Lykidis, A., Bhattencharayya, A., Bartman, A., Gardner, W., Grechkin, G.,
Lykidis, A., Bhattencharayya, A., Bartman, E., Bernal, A.,
Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,
Fonstein, M., Kyrpides, N. and Overbeek, R.
Direct Submission
Submitted (13-FEB-2002) Integrated Genomics, 2201 W. Campbell Park
Drive, Chicago, IL 60612, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Pyrimidine operon regulatory protein pyrR"
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25586"
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/EC_number="2.1.3.2"
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/gene="FN0420"
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2968. .4044
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/qene="FN0420"
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21886394
11889109
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JOURNAL
MEDLINE
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AUTHORS
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/db_xref="C1:6434497"
/db_xref="C1:6434497"
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/translation="Wassdreval"
/transla
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AKCISOOTSHINPELGGFYPAGLTPEOSNQMYTSDPVKFKKTVQNSLINGIALDIKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE010554 11942 bp DNA linear BCT 25-MAR-2002
Fusabatterium nucleatum subsp. nucleatum ATCC 25586, section 96 of
                                                                    complement(join(63978 .64270,64412 .64705,66455 .66576,66629 .66970,67242 .67534,68922 .69055,69102 .69243,69290 .69561,70362 .70488,70898 .71079))
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Fusobacterium nucleatum subsp. nucleatum ATCC 25586

Bacteria; Fusobacteria; Fusobacterium.

1 (bases 1 to 11942)

Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,

Lykidis, A., Bhattacharyya, A., Bartman, A., Gardner, W., Grechkin, G., Lu, L., Wasieva, O., Chu, L., Kogan, Y., Chaga, O., Goltsman, E.,

Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G.,

Haselkorn, R., Fonstein, M., Kyrpides, N. and Overbeek, R.

Genome sequence and analysis of the oral bacterium Fusobacterium
                                                                                                                                                                                                                                                                                                                                                       69290. .65561,70362. .70488,70898. .71079))
//gene="Ys1H4A.7"
//note="predicted using Genefinder
Contains similarity to Pfam domain: PF01175 (Urocanase),
Score=350.6. E-value=5.7e-102, N-1
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CDNA EST yk15566.5 comes from this gene
CDNA EST yk15566.3 comes from this gene
CDNA EST yk259b10.3 comes from this gene
CDNA EST yk259b10.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                    IFGIFFPRNLS1ERTRETPTAKEGDLLHNGNY
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J. Bacteriol. 184 (7), 2005-2018 (2002)
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0; Mismatches
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/gene="Y51H4A.t1"
80385. .80457
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/gene="Y51H4A.t1"
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Matches 53; Conservative
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/trānslation="mknifkDyLDIFEKYPKDEYLTKEERKERYKLLQEYEKRNYQDE
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FFKLLYDELGDRINIINKLEEFEPDYLDA TKQYYKILSNYUPESIHERWGYILLDKPI
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VDETKKRENGKKIPLDLKLHDIPNTVYSAVKGLAKFNIDILTVHAAGGSEMLKGARRAM
TEAGVWTKVTAITQLTSTSEEDEMKREQNIQTSIEESVLYARLAKESGVDGVVSSVLE
TKKIREQSGEEFIIINPGIRLAEDSKCDQKRVATPIDANRDGASYIVVGRSITGNEND
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Chareyre, P., Besson, M.T., Fourche, J. and Bosquet, G.
Identification of a Bombyx collagenous protein with multiple short domains of Gly-Xaa-Yaa repeats: cDNA characterization and regulation of expression
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/protein_id="AAL94629.1"
/db_xref="G1:19713906"
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                                                                                                           /product_"Hypothetical cytosolic protein"
/protein_id="AAL94628.1"
/db_xref="GI:19713905"
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                                                                                                                                                                                                                                                                                                                        /gene="FN0426"
9752. .10465
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/EC_number="4.1.1.23"
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230348
230348.1 GI:457768
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                                                                                               /transl_table=11
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9062. .9727
                          9062. .9727
/gene="FN0425"
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/gene="FN0427"
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/gene="FN0427"
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                                                                       /codon_start=1
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Chareyre, P.P.
Direct Submission
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/tb_xref="GI:J9713901"
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VANTAMQCILGKKLKDLGFRKDIADIGNFVSKVRPPVESFOKLKNVDTTLGPBKKSTGE
VIGTDVNLQKALYKCLFAGTKINDYSKVLFTIDDKNKEAALNLAKGFSDVGFSILTT
EGTGIYFEBYGLKKKVGKIDNSDYSVLDALQNGDVDIVINTTTKGKSSEKDGFRIRR
KATEYGVICFTSLDTANALLRVIESMSFRVQTL
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GREHVLRRPISISEIDRGENLVTITRINGECTRFMAINKRENEIDWGPLGRGYDVL
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YVSTIDGSVGTRGFTDVIKKLQAENNILVFDKYSCGPVPMIKALVNAVGEDGYISLE
NRMAGGIGACYACVCKKKKKDDYTRVCYDGPVYLASDVEIE"
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GSDIEDYYVVANKISKSPNYKALELNISCPNVKHGGIQFGTDPNVARNLTEKYKAVSS
YPYVKLSPNYTDIVAMAKAVETGGADGLTMINTLVGIVLDRKTGKPIIANTTGGLSG
PAIRRYAIRNYQQAANNIPIIGMGVWDEMDVIDFISAGASAVAUGTANFTDPFVC
PKIIDSLELALDKLGVNHILDLKGRAFR"
                                                                                                                                                                                KSISPALGRGRRVVLVDLGMKIGIVRELVSRCCDVIVVPYNTTAEEVLRLEPDGYMLT
NGPGDPEDAKESIEMIKGIINKVTIFGICMGHOLVSLACGAKTYKLKFGHRGGNHPVK
NILTGRVDITSQNHGYAVDIDSLNDTDLELTHIAINDRSCEGVRHKKYPVFTVQFHPE
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DFGIPGIYGIDTRALTRKLRSKGVVKGCLVSIDRNVDEVVAELKKTVLPTNQIEQVSS
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LAVSLHESGILDECGVEILGTKLTSIKQAEDRELFRDLMNELNEPVPDSAIVHTLEEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGVRLMPKRKDIKTILVIGSGPIIIGQAAEFDYAGTQACLSLRE
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/transl_table=11
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/gene="FN0423"
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The sequence of C. elegans cosmid EGAP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="StpC484"
                                                                       /virion
/strain="C484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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Caenorhabditis elegans
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62.8%;
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U58736.1 GI:1326297
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Miller, N.
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BOSVSSGGYOOPTYVPSTQMPPFDIYVIPFPLIYDFPGSCPCYLLMFCNNGTATNE
MQASSHPANGQSQGY APYGIIGTPVVPYVCPGNGSAMNTAQQNFPQANPVQYNCAQ
CQANRDVYRPGGRHNGARAFKELKELKSLDELNDLIRNNIKPTRTLRQIAAHPKILE
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                                                                                                                                                                                                                                                                                                   /translation="PGQGGQPIKPGQPGYPGQPGYPGQPGQPGAPGQPGQPGQPG
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Submitted (23-JUL-1996) H. Fickenscher, Universitaet
Erlangen-Nuernberg, Institut fuer Klinische und Molekulare
Erlangen-Nuernberg, Institut fuer Klinische und Molekulare
Virologie, Schlossgarten 4, D-91054 Erlangen, FRG
2 (bases 1 to 3734)
Fickenscher, H., Bokel,C., Knappe,A., Biesinger,B., Meinl,E.,
Fleischer,B., Fleckenstein,B. and Broker,B.M.
Functional phenotype of transformed human alphabeta and gammadelta
T cells determined by different subgroup C strains of herpesvirus
Submitted (03-MAR-1994) Pascal P J-M Chareyre, CGMC UMR106, Universite Claude Bernard Lyon, I, 43, Bd du 11 Novembre 1918, VILLEURBANNE, 69622, FRANCE
Location/Qualifiers
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/note="Triple helical encoding domain"
/note: Af3 a 349 t
                                                                                                 /strain="European 200x300"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%; Score 35.2; DB
65.0%; Pred. No. 1.8;
Live 0; Mismatches
                                                                                                                                                                                                                                   /product="Collagen"
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97184558
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Gammaherpeevirinae; Rhadinovirus.
1 (bases 1 to 3734)
Fickenscher, H.
                                                                                   /organism-"Bombyx mori"
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Saimirline herpesvirus 2.
Saimirline herpesvirus 2
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Matches 52; Conserv
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LEKYPPDYRKPRDLSATWDPGMPTPALPPRPANLGERQASTVRLHVKESNCKOPRER
KANBRAIVKDLKREBNKVARITCLVVVILAVLLLVTVLSILHIGMKS"
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                                                                                     /specific_host="Salmiri sclureus"
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/db_xref="taxon:10381"
/lab_host="0wd monkey kidney cells"
/note="this strain is different from strain C484 in complement(473: 1270)
/gene="TipC484"
/gene="TipC484"
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Caenorhabditis elegans cosmid EGAP7, complete sequence.
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    .3734
    /organism="Saimiriine herpesvirus 2"

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Pred. No. 2.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="StpC484"
complement(1588. .1896)
                                                                                                                                                                                                                                                                                        complement(473. .1270)
/gene="TipC484"
/codon_start=1
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INGAPPGPPGPPGPGDAGTSGQDGVPGLPGPPGPSGPGGRV
INGAPPGPPGPPGPPGPPGRDGPGPGPGPGTGGF
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Submitted (04-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
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Caenorhabditis briggsae cosmid G14K24, complete sequence.
AC084504
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Washington University Genome Sequencing Center.
The C. briggsae Genome Sequencing Project
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                                                                                                                                                                                                                                                                        Score 34.8; DB 3;
Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail: jspieth@watson.wustl.edu
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6405 c 5800 g 9884 t
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St. Louis, MO 63110, USA
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/product="tRNA-Tyr"
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1. .31110
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Caenorhabditis briggsae
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62.8%;
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Waterston, R.
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=EGAP7.1;class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
                                                                                                                                                                                                   22-MAY-2002) Department of Genetics, Washington Genome Sequencing Center, 4444 Forest Park Avenue, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.wormbase.org/db/seq/sequence?name=EGAP7;class=Sequence
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/note="coded for by the following C. elegans cDNAs:
yk289e5.3, yk327f2.3, yk327f2.5, yk289e5.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                           email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, M. 06 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="X"
/clone="EGAP7"
complement(4209: .5199)
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                                             Waterston, R.
Direct Submission
Submitted (19-MAY_1996) Robert Waterston
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                                                                                                                                                                                                 Submitted (22-MAY-2002)
                                                                                                                                                                                                                University, Genome continue. Mo 63110, USA
                           (bases 1 to 6522)
                                                                                                                         (bases 1 to 6522)
     Unpublished (2001)
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                 Louis, MO 631.
Submitted by:
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APGLRGGAGEPGKNGAKGEPGPRGERGEAGIPGVPGAKGEDGKDGSPGDPGANGLPGA
AGERGALGSRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPGRDGVPGGPGMRGMP
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GNPGPPGPSGSPGKDGPPGPAGNTGAPGSPGVSGPKGDAGQPGEKGSPCAQGPPGAPG
PLGIAGITGARGLAGPPGMPGPRGSPGPQGVKGESGKPGANGLSGERGPPGFQGLPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence overlaps with that reported by Chu et. al. in J. Biol. Chem. 260:4357-4363(1985), by Toman et. al. in Nucl. Acids Res. 16:7201-7201(1988) and by Mankoo et. al. in Nucl. Acids Res. 16:2337-2337(1988).
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GSPGSPGYQGPPGEPGQAGPSGPPGPPGAIGPSGPAGKDGESGRPGRPGDRGLPGPPG
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GRGGPQPQPGPGKNGEYGPORPGPGGPGPGPRGPGPGACGAGGLGCLFGGPPGGPPGPRG
PGEPGPRGARAPGGKGDAGAPGERGPPGLAGAPGLRGGAGPPGPEGGKGAAGPP
GPPGAAGTPGLQGMPGERGGLGSPGPKGDKGEPGGPGADGVPGKDGPRGPTGPTGPPG
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SPGPAGQQGA IGSPGPAGPRGPVGPSGPPGKDGTSGHPGP IGPPGPRGNRGERGSEGS
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Janeczko, R. and Ramirez, F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-MAY-1989) Janeczko R., Ramirez F., Suny Health
Science Centre, 450 Clarkson Avenue - Box 44, Brooklyn NY 11203,
17444 GCTGGATCCCCAGGACCAGCAGCATCCAGGAAACGCCGGAGCTCCAGGAACCCCAGGA 17385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3234)
Janeczko, R.A. and Ramirez, F.
Nucleotide and amino acid sequences of the entire human alpha
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                                                                                                                                                                                                                           HSC3A1R 3234 bp mRNA linear
Human COL3A1 mRNA for pro alpha-1 (III) collagen.
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89386015
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/db_xref="taxon:9606"
/map="2q31"
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Search completed: February 20, 2003, 04:31:48 Job time : 500.581 secs
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Title: Perfect score:

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499 bp mRNA linear EST 20-MAR-2002 LMZ4HW0134 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone LM-24 HW-011-34 (5'), mRNA sequence.
             BE079777 RCG-BT062
BE079777 RCG-BT062
BR019876 RCG-BT062
AW813783 RC3-57019
AV731140 AV731140
BE42042 3 2-393 hu
A0012504 CTT-HSP-2
BF881529 QV1-ET018
A0013990 Pan trog1
BL180953 TY4F01 he
AW517269 EST84499
AG019007 Homo sap1
BC19007 Homo sap1
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BC19008 Homo sap1
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AG16883 AV716883
BC2900 MR1-HN006
BF82806 MR1-HN006
BF82806 G01285954
AG080755 Pan trog1
BC729218 G01285954
AG080755 Pan trog1
BC72956 G01669973
BC728976 G01669973
BF72897 G01669973
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Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Comckchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhycon@rda.go.kr
Insert Length: 499 Std Error: 0.00
Seq primer: CAGGAAACAGCTATGAC
POLYA-NO.
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                     /tissue_type="longissimus dorsi"
/cell_type="myocyte"
/dev_stage="24 months old"
/lab_host="xL1-BlueMRF'strain"
/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1:
ECORI; Site_2: Xho I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 GGTCTTCACATGCAGGGTGCCAGGAAATTACCATTTCCTTTTCTATGTGGATCTCCATCA 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 AGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCCAGCTTTGATGTTGAGCTGCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 113.6; DB 14; Length 499;
                       /db_xref="taxon:9913"
/clone="LM-24-HW-011-34 (5')"
/clone=llb="Bos taurus LM-24-HW cDNA library"
/sex="six males mixed"
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.4e-21;
/organism="Bos taurus"
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64.28;
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Contact: Smith TPL
USDA, ARS. US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4360
VO. 980904. Sequencing. Bases called and alt_trimmed with phred
vo. 980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211669 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
BE757276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    adrenal, and endometrium.
131 c 146 g 128
                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
PCR PRIMERS
FORWARD: AGGAACAGTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 63 row: G column: 13
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                          Location/Qualifiers
1. .504
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189
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AA777621/C
LOCUS
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGO88117 612 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-086P15.F, genomic survey sequence.
AGO88117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sali; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and dometrium."
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 612)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 76.4; DB 12; Length 526; 61.6%; Pred. No. 1.2e-10; tive 0; Mismatches 76; Indels 0
                                                                                                                                /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC Library clone:PTB-086P15.F.
Pan troglodytes
            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 63 row: G column: 14
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                    /organism="Bos taurus'
                                                                              Location/Qualifiers
FORWARD: AGGAAACAGCTATGACCAT
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Matches 122; Conservative
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AG088117
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/sex="male"
//dev_stage="20 week-post conception fetus"
//dev_stag
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Walte, Y., Wylle, T., Waterston, R. and Wilson, R. Gupublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA777621
z195a07.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lamage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 GAACTITGAACTIGAGAGAGATCATTTAGGGTATCAGGAGGAGAAATTTCTAAGCAGCA 328
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/organism="Homo sapiens"
/db_xref="GDB:1352557"
/db_xref="taxon:5606"
/clone="IMAGE:448500"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 612;
                                                                                                                                                                                                                                                                                                                                              /clone_lib="PTB Chimpanzee Male BAC Library" | 111 c 163 q 149 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61.8; DB 17;
Pred. No. 1.7e-06;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 AAGCATTCAAGAGTTGACTTGGGTGCTGTTAAAGGCA 365

    .612
    /organism="Pan troglodytes"
    /db_xref="taxon:9598"
    /clone="PTB-086P15.F"

R.Site 2 : SacI.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            element;, mRNA sequence.
AA777621
AA777621.1 GI:2837100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%;
illarity 77.3%;
Conservative
                                                                                                                                                                                                                                                                                                     /sex="male"
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Best Local Similarity
Matches 75; Conserv
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Gaps

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24; Indels

0; Mismatches

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73; Conservative
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Best Local Similarity
Matches 73; Conserv
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BE079777.1
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BE079777/c
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  Matches
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KEYWORDS
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-BT0254-220
300-019-c05&t3=2000-03-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 440.

Location/Qualifiers
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
  Library
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                                                                                                                                                          Gaps
                                                                                                                                                                                            334 CTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAA 393
                  went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
and Eco RI sites of the modified pT7T3 vector.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                   Length 538;
                                                                                                                                                                                                                                                                                               118 GAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA
                                                                                                                                                          34; Indels
                                                                                                               Score 59.6; DB 9;
Pred. No. 6.5e-06;
0; Mismatches 34;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BP0254"
/dev_stage="Adult"
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BE062167.1 GI:8406817
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75.3%;
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Best Local Similarity

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EST 12-JUN-2000
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126 c 86 g 146 t 1 others
351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                            237 GAACTTTGAACTTGAGAGAGAGATTTATGGTATCTGGCAGAAGAAATTTCTAAGCAGCA 178
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/clone_lib="CIT Human Genomic Sperm Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, MA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: Kzackroneu, washington.edu
Sequence Tagged Connector
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Pred. No. 1.2e-05;
                                                                                         411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707012
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-BT0627-140
200-011-A05&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 69
High quality sequence stop: 537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 2 others
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RC6-BY0627-220300-012-H08 BY0627 Homo sapiens CDNA, mRNA sequence.
BE079876
                                                                      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia; G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
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                      Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                 Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Euthería; Primates; Catarrhini; Hominidae;
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/organism="Homo sapiens"
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/clone_lib="BT0627"
/dev_stage="Adult"
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                                                                            AUTHORS
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-BT0627-220
300-012-H08&t3=2000-03-22&t4=1)
Seq primer: puc IB forward
High quality sequence start: 32
High quality sequence stop: 563.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Slmpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             Sao Paulo-SP,
  Jongeneel, C.V., O'Hare
                                                                    expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 GAATATTTGCCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J.
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                                          \operatorname{Simpson}, \operatorname{A.J.} Shotgun sequencing of the human transcriptome with ORF
                                                                                                            U.S.A. 97 (7), 3491-3496 (2000)
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Pred. No. 1.3e-05;
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                                                                                                          Proc. Natl. Acad. Sci.
20202663
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ilarity 75.3%;
Conservative
                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                        144 C
                                                                                                                                                                                                                                                  73; Conservative
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I (Dases 1 to 727)

E (Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu, S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,Z. and Han,Z.

L (Oppublished (2000)

Contact: Zequang Han Chines Chines Chinese National Human Genome Center at Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)
                                                                                                                          Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0197-120
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Seq primer: puc 18 forward
High quality sequence start: 23
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Location/Qualifiers
Location/Qualifiers
1. 678
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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Site_2: Smal: A mini-library was made by cloning products
Site_3: Smal: A mini-library was made by cloning products
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRAA and cDNA amplification were performed under
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                                                           Sao Paulo-SP,
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                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58.6; DB 10;
Pred. No. 1.4e-05;
); Mismatches 24;
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174 c 108 g 234 t
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 Contact: Simpson A.J.G.
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                                                                                            Tel: +55-11-2704922
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                                                                           Brazil
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AV731140
LOCUS
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Lu, X., Cui, L. and Li, Y.
DDRT-PCR from B cell
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: xingwu Lu,liangxian Cui,yonghai Li
Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Bacchemistry
Institute of Basic Medical Science, Peking Union Medical College
Dongban Sanriao 5, Beijing, P.R.C, 100005
Tel: 86-010-65296551
Email: luxingwu@263.net
full-length and coding sequence.
                                                                                                                                                                                                                               351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                                                                                                                                                                                                                                      351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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                                                  11 others
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                                                                                                                                                                            24;
                                                                                                                       Score 58.6; DB 10;
Pred. No. 1.4e-05;
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BE420422.1 GI:16041640
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DEFINITION

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ACCESSION

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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1. .345
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stingency conditions."
                                                                                                                                                                                                                                                                                                                    Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-ET0181-
031200-546-f03&t3-2000-12-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 89.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:si81-45-503-9117)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                     Shotgun sequencing of the human transcriptome with ORF expressed
     Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                    U.S.A. 97 (7), 3491-3496 (2000)
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Pan troglodytes DNA, clone: PTB-094J23.R,
AG093990
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                                                                                                 Proc. Natl. Acad. Sci.
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Fax: +55-11-2707001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 345)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., ad silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Ragal,M.A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                        AQ012504 342 bp DNA linear GSS 06-JUN-1998
CIT-HSP-2298M4.TF CIT-HSP Homo sapiens genomic clone 2298M4, DNA
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 342)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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Seq primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random BAC End Sequence Database for Sequence-Ready Map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447
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100.0%; Pred. No. 1.5e-05;
1ve 0; Mismatches 0;
553 AAGCATTCAAGAGGTAACTTGGGTGCTGTTAAAGGCA 589
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/db_xref="GDB:7153856"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AQ012504.1 GI:3185069
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FEATURES

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Gaps

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Length 345; Indels 03-NOV-2001

linear GSS 03-NOV-200 genomic survey sequence.

RESULT 14 BF881529/c DEFINITION

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ACCESSION

VERSION

REFERENCE AUTHORS

BASE COUNT

ORIGIN

Matches

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clone tracking errors.

PRIMERS

Sequencing: M13Rev
LIBRARY

Vector : pkS145

R.Site 1 : SacI.

R.Site 2 : SacI.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Aclone="Prb-094J23.R"

/ clone="Prb-094J23.R"

/ clone="Prb-094J23.R"
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8932, Ap 24780, A

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Sequence 83, Appl.
Sequence 8787, Ap
Sequence 8034, Ap
Sequence 9454, Ap
Sequence 9454, Ap
Sequence 9454, Ap
Sequence 7495, Ap
Sequence 7399, Ap
Sequence 7399, Ap
Sequence 7444, Ap
Sequence 7441, Ap
Sequence 3449, Ap
Sequence 3449, Ap
Sequence 256, Ap
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Sequence 6, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 3, Appli
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APPLICANT: FOX, Brian
APPLICANT: HOLloway, James L.
ATTLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-835-232-7
US-09-864-761-8932
US-09-864-761-8932
US-09-864-761-8932
US-09-864-761-89334
US-09-864-761-8934
US-09-864-761-8934
US-09-864-761-9945
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US-09-864-761-7556
US-09-864-761-74411
US-09-864-761-756
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Best Local Similarity 100.0%; Pred. No. 3.1e-130;
Matches 447; Conservative 0; Mismatches 0;
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  NAME/KEY: CDS
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Sequence 3, Appli
Sequence 7, Appli
Sequence 15057, A
Sequence 2107, Ap
Sequence 21786, Ap
Sequence 3115, Ap
Sequence 3115, Ap
Sequence 11516, A
Sequence 2508, Ap
Sequence 2508, Ap
Sequence 2508, Ap
Sequence 341, Ap
                                                                                              February 19, 2003, 18:01:21; Search time 35.9695 Seconds (without alignments) 6329.459 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*
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Compugen Ltd
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US-09-960-352-9137
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US-09-960-352-1786
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US-09-960-352-4241
US-09-864-761-25080
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US-09-819-607-3
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US-09-864-761-8643
US-09-864-761-8938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-997-610-1
US-09-997-610-5
US-09-997-610-3
US-09-997-610-7
                                                                                                                                                                                                                                                           424239 seqs, 254661826 residues
              version:
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                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      nucleic search, using sw model
                                                                                                                                                        US-09-997-610-1_COPY_2_448
                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
              GenCore
Copyright (c) 1993
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seq length: 2000000000
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Match Length 1
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                                                                                    301 CCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGAATATTTGG 360
                                                                                                                                    361 CTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAAAGCATTCAA 420
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APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
CURRENT PELLING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRASEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 3.5e-130;
ive 0; Mismatches 0;
                                                                                                                                                                                  Sequence 5, Application US/09997610
Patent No. US20020156244A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 447; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)...(1731)
US-09-997-610-5
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                                                                                                                                                                                                                                                            09-997-610-5
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                   61 CCAGCACACCCCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAA 120
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                                                                                                                                                                                                                                                                                      APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRPI3
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                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                    421 GAGGTGACTTGGGTGCTGTTAAAGGC 446
                                                                                                                                                                                                                            Sequence 3, Application US/09997610 Patent No. US20020156244A1 GENERAL INFORMATION:
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LOCATION: (1)...(1377)
OTHER INFORMATION: Each n is ind
MAME/KEY: misc_feature
LOCATION: (1)...(1377)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 1377
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GENERAL INFORMATION:
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OTHER INFORMATION: of SEQ ID NO:6
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                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
TILLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.5%; Score 324.2; DB 9; Best Local Similarity 61.0%; Pred. No. 1.2e-91; Matches 272; Conservative 95; Mismatches 79;
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/997,610 CURRENT FILING DATE: 2001-11-29 PRIOR APPLICATION NUMBER: US 60/253,924 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15057, Application US/09960352
Patent No. US20020137139A1
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CCATION: (1)...(1731)

OTHER INFORMATION: n = A,T,C or G

US-09-997-610-7
                                                                                         Sequence 7, Application US/09997610 Patent No. US20020156244A1
ORGANISM: Artificial Sequence FEATURE:
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 GTCCGCCTTCACTGTGAAGCTCAGTGGCCAATTGCCGTCCCCTTCAAAGCCTGTGCCCTT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAAGGAGGCCATGGGAGTCTTTGCTTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         25.7%; Score 114.8; DB 10; Length
72.3%; Pred. No. 2.7e-26;
iive 0; Mismatches 57; Indels
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Pred. No. 1.2e-19;
0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB34-018-Q1-E1-B12
US-09-960-352-9137
                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; OGGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 64-LIB34-036-Q1-E1-H8
US-09-960-352-15057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9137, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 62.7%;
Matches 163; Conservative
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Best Local Similarity 72.3
Matches 149; Conservative
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GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3715
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCCCTGT 159
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                                                                                                                                                                                                                                                                                                              46 GAAGITGCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCA 105
                                                                                                                                                                                                                          106 CCAGGTTTACCACAATATACAGGAG---AAATAAGTGAAATGACAAAATGCCCCTGTCCT 162
                                                                                                                                                                                                                                                                                                                                                                                                                  266 TGCCACAGACAGTCCGCCTTCACTGTGAAGCTCAGTGGCCAGTTGCCTTCCCCTTCAAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGA 282
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                                                                                                                                                                                                                                                                                                                                                                         163 GATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCAAG
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                                                                                                        Length 392;
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16-LIB34-049-Q1-E1-D11
                               ; OTHER INFORMATION: Clone ID: 08-LIB34-023-01-E1-B7 US-09-960-352-1786
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                                                                                                      Score 82.8; DB 10;
Pred. No. 2.8e-16;
0; Mismatches 92;
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0; Mismatches 148;
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US-09-960-352-3715
Sequence 3715, Application US/09960352
; Patent No. US20020137139A1
                                                                                                        Query Match 18.5%;
Best Local Similarity 61.4%;
Matches 151; Conservative
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Clone ID:
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Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bos taurus
                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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386 GTTCTT 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 GTCTTT 288
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                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Sequence 1786, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
PAPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
GURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1786
LENGTH: 392
                                                                                                                                                                                                                                                                                                                         Sequence 220, Application US/09960352
Patent No. US2002013139A1
GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nangbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERBNCE: 16511.006/37-21.10289.C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DAIE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
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                        276 TGCCACAGACAGTCCGCCTTCACTGTGAAGCTCAGTGGCCAGTTGCCTTCCCCTTCAAAG 335
                                                                                                          61 CAGGGTGCCAGGAAATTACCATTTCCTCTTTGATGTGGATCTCCATCACTGCAAGGTGAC 120
                                                                                    223 CCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATGGGA 282
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163 GATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTCAAG 222
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COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: 01-LIB34-084-Q1-E1-A9
US-09-960-352-220
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Pred. No. 4.8e-19;
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76.7%;
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Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
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Sequence 4241, Application US/09960352
Sequence 4241, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: UNGRES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                          Length 447;
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; OTHER INFORMATION: Clone ID: 18-LIB34-077-01-E1-E5
US-09-960-352-4241
      ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 16-LIB34-024-Q1-E1-D7
US-09-960-352-3684
                                                                                                                                    Score 73.2; DB 10;
Pred. No. 3.1e-13;
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%; Score 60.6; DB 10;
ilarity 54.5%; Pred. No. 2.8e-09;
Conservative 0; Mismatches 115;
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                                                                                                                                    Ouery Match
Best Local Similarity 60.6%;
Matches 120; Conservative
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ORGANISM: Bos taurus
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Best Local Similarity
Matches 145; Conserv
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LOCATION: (377)
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APPLICANT: Tao, Neighing
APPLICANT: Tao, Neighing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NOS: 15112

**ABBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tale, Nengbing APPLICANT: Tale, Nengbing APPLICANT: Tale, Nengbing APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. Tale Color in Mathematical Math
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
174 GTCAGCCTTTACTGTGAAGCTCAGTGGAAACTTCCTCTTCCTTTCAAGCCCATCATT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 CACAGGGTCCTGTACAATGCCCAGAGGATTTAAAGGAGGCCATGGGAGTCTTTGCTTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 CAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGAA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 49-LIB34-046-01-E1-E2
                                                                                                                                                                                                                            340 CATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATT 378
                                                                                                                                                                                                                                                                    299 CAGCATGCTGTGAAGCTAGGGCTCATGAAGAATGACACT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.0%; Score 76; DB 10; 60.8%; Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11516, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3664, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 TATTTGGCTAATGAGGAAGCAAAT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.8
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-960-352-11516
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-960-352-11516
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GENERAL INCORRATION

APPLICANT: Renk, David R.

APPLICANT: Renk, David R.

APPLICANT: Haraci, David R.

APPLICANT: Haraci, David R.

APPLICANT: Haraci, David R.

APPLICANT: Haraci, David R.

TITLE OF INVENTION: EDRINGLE EXON NUCLEIC ACID PROBES USEFUL FO ITITLE OF INVENTION: EDRE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT FILLE OF INVENTION: EDRE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT FILLE OF DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US (05/43, 366

PRIOR PLILIC BATE: 2000-06-03

PRIOR PLILIC BATE: 2000-01-04

PRIOR PLILIC BATE: 2000-01-04

PRIOR PLILIC BATE: 2000-01-04

PRIOR PLILING DATE: 2000-01-04

PRIOR PLILING DATE: 2001-01-04

PRIOR PRILING DATE: 2001-01-04

PRIOR PLILING DATE: 2
                                                                                                                                       348 GGTGAATATTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
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0
Length 273;
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7
                                                                                                                                                                                                                                                                           Score 58.4; DB 10;
Pred. No. 1e-08;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8349, Application US/09864761 Patent No. US20020048763A1
   13.18;
74.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US C
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                Best Local Similarity 74.0
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-864-761-8349
   Query Match
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SHATCON G.
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NN: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7

NN: EXPRESSED IN HETA, SIGNAL = 6.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 2

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

NN: EXPRESSED IN HEART, SIGNAL = 5.5

NN: EXPRESSED IN PLACEMYA, SIGNAL = 5.5

NN: SMISSPROT HIT: P29539, EVALUE 6.80e-01

NN: SMISSPROT HIT: BE16318.1, EVALUE 3.00e-78

NN: NT HIT: AL163210.2, EVALUE 7.00e-75
                                                                                                                                                                 Sequence 25080, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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438 GGAGTGTTCACCTGCACCATCCCTGG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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                                                                                                              N: EXPRESSED IN PLACENTA, SIGNAL = 20
N: EXPRESSED IN BRAIN, SIGNAL = 14
N: EXPRESSED IN HELA, SIGNAL = 15
N: EXPRESSED IN HELA, SIGNAL = 13
N: EXPRESSED IN HEATO, SIGNAL = 12
N: EXPRESSED IN HEATO, SIGNAL = 12
N: EXPRESSED IN PETAL LIVER, SIGNAL = 13
N: EXPRESSED IN FETAL LIVER, SIGNAL = 14
N: EXPRESSED IN LUNG, SIGNAL = 14
N: EXPRESSED IN LUNG, SIGNAL = 14
N: EXPRESSED IN BONE MARROW, SIGNAL = 14
N: EXPRESSED IN BONE MARROW, SIGNAL = 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 10;
Pred. No. 8.3e-08;
0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AAGCATTCAAGAGGTGACTTGGGTACTGTTAAAGGCA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%;
74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.8 Best Local Similarity 74.2 Matches 72; Conservative
                                                                    ORGANISM: Homo sapiens
                                                                                                              OTHER INFORMATION: E OTHER INFORMATION: E
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) OTHER INFORMATION:
US-09-864-761-2925
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                      348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                   DB 10; Length 519;
                                    = 2
= 1.8
                                                                                                                                                                                             Score 58.4; DB 10; Length
Pred. No. 1.5e-08;
0; Mismatches 26; Indels
  D IN HELA, SIGNAL = 6.1
D IN ADULT LIVER, SIGNAL = 1
D IN BONE MARROW, SIGNAL = 1
D IN HEART, SIGNAL = 5.5
D IN PLACENTA, SIGNAL = 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annomax Sequence Listing Engine vers. 1.1
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CURRENT PELLING DATE: 2001-05-23

PRIOR FILING DATE: 2001-05-23

PRIOR FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-03

PRIOR PELLING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2000-09-21

PRIOR PRILING DATE: 2000-09-21

PRIOR PRILING DATE: 2000-09-21

PRIOR PRILING DATE: 2000-09-21

PRIOR PRILING DATE: 2000-09-21
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                                                                                                                                                                                                13.1%;
74.0%;
; OTHER INFORMATION: EXPRESSED; OTHER INFORMATION: EXPRESSED; OTHER INFORMATION: EXPRESSED; OTHER INFORMATION: EXPRESSED US-09-864-761-8349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence I
SEQ ID NO 2925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                      74; Conservative
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-864-761-2925
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ALIGNMENTS

Sequence 3 Sequence 3 Sequence 3

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ATGTAGAAGTTGCTGGACCTCCAGCACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTG 100
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Pred. No. 7.4e-06;
0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/463,911
US-08-991-789A-141

US-09-062-451-141

US-09-052-141

US-08-092-770-8

US-09-223-992A-7

US-08-997-221-37

US-08-977-221-37

US-08-977-221-37

US-08-977-221-37

US-08-977-221-37

US-08-977-221-35

US-09-483-818-35

US-09-483-818-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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STREET: TWO ...
CITY: Lexington
~~***TE: Massachusetts
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Best Local Similarity 48.8
Matches 164; Conservative
   nucleic acid
EDNESS: single
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   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-463-911-6
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Sequence 3, Appli
Patent No. 5171840
Patent No. 5480796
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Sequence 217, App
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
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59, Appl
5, Appl
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Patent No. 5171840
Patent No. 5480796
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                                                                                                                          February 19, 2003, 16:09:30; Search time 29.509 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                                                                101 GTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCCCTGTC 160
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APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
TILE REFERENCE: 97-49
CURRENT PAPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER APPLICATION NUMBER: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.4e-05;
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Patent No. 6197930
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LENGTH: 4517
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                                            GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Marison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington CITY: Lexington CATA: USSACHUSETTS COUNTRY: USA
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Pred. No. 0.00058;
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                                                                                                                                                                                                                                FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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FILING DATE: US/08/463,911
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
Sequence 217, Application US/09188930A Patent No. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM
TITLE OF INVENTION: EXCLOSIVELY IN
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Patent No. 5869330
GENERAL INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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Best Local Similarity
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SEQ ID NO 217
LENGTH: 1107
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; ORGANISM: Rat
US-09-188-930-217
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US-08-463-911-1
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205 CTTCCTCTTCCATCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGAT 264
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Pred. No. 0.026;
0; Mismatches 81; Indels 0
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                                                                                       Sequence 1, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %3-09-140-804-1; Sequence 1, Application US/09140804; Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%;
Best Local Similarity 51.5%;
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.4%;
ilarity 51.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (198)...(926)
... US-09-140-804-1
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-336-536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1347
                                                                   US-09-336-536-1
                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 CTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTTCA 220
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                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1276;
                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2; Length 127
Pred. No. 0.0037;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 GATGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
ATTLE OF INVENTION. SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 CATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAA 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557 TGAAAGATGTGAAGGTGAGCCTCTTCAAGAAGGACA 592
                             WHI95-05
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US-09-336-536-2
; Sequence 2, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.1%;
Matches 106; Conservative
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Best Local Similarity
Matches 86; Conserv
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; LOCATION:
US-08-463-911-1
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603 TACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGGTCTACTTCGCCGTC 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 GGNMGNCCNGGNYTNCCNGGNCCNMGNGGNGAYCCNGGNCCNMGNGGNGARGCNGGNCCN 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ACTGTGAAGCTCAGTGGAAAACTTCCTCTTTCCAAGCCCATCATCTTCACAGGGGTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 AARMGNWSNGARWSNMGNGTNCCNCCNCCNWSNGAYGCNCCNYTNCCNTTYGAYMGNGTN 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 YTNGTNAAYGARCARGGNCAYTAYGAYGCNGTNACNGGNAARTTYACNTGYCARGTNCCN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 GGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GCACACCCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39; OTHER INFORMATION: polypeptide of SEQ ID NO:2.
US-09-140-804-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 729;
                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
APPLICANT: Homes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS.
TITLE NOT INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS.
FILE REFERENCE: 197-49
CURRENT FILING DATE: 1990-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER PILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 36.2; DB 4; Length 7; Pred. No. 0.047; 33; Mismatches 189; Indels
                                                                   325 GATGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SPINELLA, Dominic
APPLICANT: BECHERER, Kethleen
APPLICANT: BECHERER, Kethleen
TITLE OF INVENTION: SCHOOL STATLE OF INVENTION: SCREENING DRUG LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen-Probe Incorporated
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                                                                                                                                                                              Sequence 10, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.1%;
Best Local Similarity 27.9%;
Matches 86; Conservative 3
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505 GTNAARAA 512
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70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATACCTGTCTTAATAACGCCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
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5171840-8
;Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.8; DB 2;
Pred. No. 0.077;
0; Mismatches 62;
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                                                                                                                      SOFTWARE: FESTEM: DOS
SOFTWARE: FESTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DAMP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 35.8; DB 54.1%; Pred. No. 0.088;
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10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298,694
FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                          36,510
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CB TELECOMMUNICATION INFORMATION: TELEPHONE: 619-410-8926
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%;
54.1%;
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.18;
                                                                                                                                                                                                           03-APR-1996
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 54.19
Matches 73; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
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                                                                                                                                                                                                                FILING DATE: 03-APR-CLASSIFICATION: 435
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Matches 73; Conserv
                    San Diego
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                                                     USA
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LENGTH: 1404
                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-627-151A-15
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDED: ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
                                                                                                                                                                                                                                  Length 1486;
                                                                                                                                                                                                                              8.0%; Score 35.8; DB 4; Length 14
54.1%; Pred. No. 0.091;
tive 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS BOITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICR APPLICATION DATA:

APPLICATION NUMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1037
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09439856 Patent No. 6410009
                   TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1486 base pairs
TYPE: nucleic acid
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
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Best Local Similarity 54.18
These 73; Conservative
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STRANDEDNESS: single
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STATE: New York
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US-08-795-473B-3
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US-09-439-856-3
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APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0%; Score 35.8; DB 6; Length 1404; Best Local Similarity 54.1%; Pred. No. 0.088; Matches 73; Conservative 0; Mismatches 62; Indels 0
                                                                                                                                                                                                Patent No. 5480796

PAPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

FOR HUMAN B CELL STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:

PELLING DATE: 02-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 298,694

FILING DATE: 19-JAN-1989
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/795,473B
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NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
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MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08795473B Patent No. 6217858
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FILING DATE: 11-FEB-1997
                                                           130 GAAATAAGTGAAATG 144
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RY: USA
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US-08-795-473B-3
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COUNTRY:
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5480796-8
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8.0%; Score 35.8; DB 4; Length 1486; illarity 54.1%; Pred. No. 0.091; Conservative 0; Mismatches 62; Indels 0
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8.0%; Score 35.8; DB 6; Length 2061;
Best Local Similarity 54.1%; Pred. No. 0.11;
Matches 73; Conservative 0; Mismatches 62; Indels 0
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Patent No. 1818HMOTO, TADAMITSU

TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

FOR HUMAN B CELL STITULIATORY FACTOR-2

NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:

PILING DATE: 02-JUL-1992

PRIOR APPLICATION NUMBER: 298,694

FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels
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Patent No. 5171840

Patent No. 5171840

Patent No. 5171840

Patent OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

RPLICATION NUMBER: US/07/298,694

FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.8; DB 6;
Pred. No. 0.11;
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Best Local Similarity 54.1%;
Matches 73; Conservative
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Human genome-derlv
DNA encoding novel
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Human brain expres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Probe
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/note= "No stop codon is given"
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AAK34535
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                            2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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AAI26826
AAIS6100
ABA62555
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                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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519
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Match I
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13.1
13.1
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Sequence:
                                                                                                                                                                                                                   Scoring table:
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0B DB

Minimum Maximum

Database

126459786

Result Š.

Searched:

bone marrow #7875 for ge #11614 used

99US-0122487

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21-FEB-2000; 2000EP-0200610.
                                                                                                                                                 (GEST ) GENSET
                                                                                                                26-FEB-1999;
              EP1033401-A2.
                                               06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                               impaired glucose tolerance, insulin resistance; Syndrome X; Type II diabetes, hyperlipidaemia; atherosclerosis; hypertension; and heart diseases (e.g. cardiac insufficiency, coronary insufficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present CDNA
                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                    or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TGGAATGTCCTGGTGCCCCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AGGAGGCCATGGGAGTCTTTGCTTGCATGCGTGCCTGGGAATTACTACTCCAGCTTTGATG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 TTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 TGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAACTTC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 CTCTTCCTTTCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 TTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATA 388
                                                                                                                                                                 obesity, impaired glucose tolerance, insulin resistance, Syndrome X, Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1338 BP; 359 A; 288 C; 350 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ر.
ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 351; DB 24;
Pred. No. 2.5e-103;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 28426.
                                                                              ij
                                                                              Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence encodes the human GMG-9 protein.
                                                                                                                                                                                                                                    Disclosure; Page 122-124; 128pp; English.
                                                                              'n
                                                                              Bihain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC24351 standard; cDNA; 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.5%;
ilarity 98.6%;
Conservative
            16-JAN-2001; 2001US-262235P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                              Bour BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                              WPI; 2002-557821/59.
                                                                                                                                P-PSDB; AA015423
                                             (GEST ) GENSET
                                                                              Erickson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #23381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 404 BP; 137 A; 55 C; 101 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 58.6; DB 21; 75.3%; Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
   Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 28426; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA75076 standard; DNA; 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
Dumas Milne Edwards J,
                                                             WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA75076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ABA75076
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, e.g. cardiovascular diseases of the human heart and vascular system congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                               Single exon nucleic acid probes for analyzing gene expression in human hearts \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58.4; DB 22; Length 273;
Pred. No. 1.2e-08;
0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 23582.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID No 18226; 530pp; English
                       DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                       Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 74.0
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG, Hanzel DK,
                       Hänzel DK,
                                                          WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK23591
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0
                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GGGGAACATTGAACTTGAGAGAGATGATTTGGGGTATCTGGTGGAAGAAATTTCTAAACA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #18226 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 273;
                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 23381; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.4; DB 22;
Pred. No. 1.2e-08;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                    Rank DR;
                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%;
74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                   21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
2000US-0608408
2000US-0632366
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 74.0 tes 74; Conservative
                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                       WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157274-A2
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA39760;
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Matches
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Sequence 273 BP; 80 A; 36 C; 81
such as lymphoma, leukaemia
the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                              AAI26826;
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                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe;
                                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one . The probes of the
             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                         Example 4; SEQ ID NO: 23582; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow expressed single exon probe SEQ ID NO: 24276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 24276; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                Length 273;
                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                                                                                                                                                Score 58.4; DB 22;
Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          408 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
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26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0633266.
03-AUG-2000; 2000US-0234687.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-02369.
                                                                                                                                                                                                                                                 13.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK49719 standard; DNA; 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                               74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488900/53
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK49719;
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                                                                                                                                                                                                                                                 Query Match
                             brains
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directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #16759 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC
                                                                                                     348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                   ;
0
     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing gene expression in human cervical epithelial cells
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                                                   Indels
                                                                                                                                                                                                        GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                            175 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 214
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Pred. No. 1.2e-08;
Score 58.4; DB 22;
Pred. No. 1.2e-08;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                            Pred. No. 1.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 16759; 487pp; English
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                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0207456.
2000US-0608408.
2000US-0632366.
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74.0%;
Match 13.1%;
Local Similarity 74.0%;
nes 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                273
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer; ss
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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standard; DNA;
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                                                                                                                                 Homo sapiens
                                                           01-FEB-2002
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                                      ABA62555;
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              ABA62555
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ABA62555
ID ABA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                         Probe #24296 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                      348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for
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   26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Indels
                                                                                                                                                                                                                                                 microarray; human; placenta; antenatal diagnosis;
                                                                                  GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 273 BP; 80 A; 36 C; 81 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human placenta
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 24296; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                    (first entry)
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                             genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                                                          40200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                    Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                   17-0CT-2001
 74;
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                                                                                                                                                                            AAI55610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                  Probe;
                          348
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  Matches
                                                                      408
                                                                                            175
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                                                                                                                               RESULT 8
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foetal liver; gene expression; single exon nucleic acid probe; ss.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 GGGGAACATTGAGAGAGAGATTTGGGGTATCTGGTGGAAGAATTTCTAAACA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #8349 for gene expression analysis in human heart cell sample.
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Pred. No. 1.7e-08;
0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 10860; 639pp + sequence listing; English.
                                                        Human foetal liver single exon nucleic acid probe #10860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid r
analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
04-OCT-2000; 2000GB-0024263.
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74.0%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
Human; gene expression; heart; microarray; vascular system; probe; cardlovascular disease; hypertension; cardlac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 58.4; DB 22; Length 519; 74.0%; Pred. No. 1.7e-08; ive 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe SEQ ID NO: 10902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 GCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 8349; 530pp; English.
                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK10911 standard; DNA; 519 BP
                                                                                                                                        04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-033366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                          Chen W,
                      congenital heart disease; ss
                                                                                                                   30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease.
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nes 74; Conservative
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                                                                    WO200157274-A2
                                               Homo sapiens
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                                                                                            09-AUG-2001
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.1%; Score 58.4; DB 22; Length 519; 74.0%; Pred. No. 1.7e-08; Live 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGATAAAGGCA 353
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                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
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2000US-0234687.
2000US-0236359.
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2000US-0207456.
2000US-0608408.
                                                                                                  30-JAN-2001; 2001WO-US00667
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2000US-0207456
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nes 74; Conserv
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WO200157275-A2.
                                                                                                                                                                                                                          03-AUG-2000; 21-SEP-2000; 27-SEP-2000;
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                                                                                                                                                                           26-MAY-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging off diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #11227 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                   348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells .
                                                                                                                                                                                                                                                                          y Match 13.1%; Score 58.4; DB 22; Length 519; Local Similarity 74.0%; Pred. No. 1.7e-08; hes 74; Conservative 0; Mismatches 26; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           314 GCAAAGCATTCAAGAGGTGACTTGGCTGCTGTTAAAGGCA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 11227; 654pp; English.
                                                           Claim 25; SEQ ID No 7554; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687,
24-SEP-2000; 2000US-0234687,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder; ss
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                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #7554 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                  348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 GGGGAACATTGAACTTGAGAGAGGATTTGGGGTATCTGGTGGAAGAAATTTCTAAACA 313
                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                               present invention provides a number of single exon nucleic acid
                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                 Example 4; SEQ ID NO: 11326; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                          Score 58.4; DB 22; Length 519;
Pred. No. 1.7e-08;
0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
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                                                                                                                 Rank DR;
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                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                 Chen W,
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             ; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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74.0%;
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                    the probes of the invention.
  2000US-0608408
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2000US-0608408.
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                                                                                                                 DK,
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                                                                                                                                            WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer; ss
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                 Hanzel
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                           27-SEP-2000;
04-OCT-2000;
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The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                         348 GGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCA 407
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                                                                                                        . Match 13.1%; Score 58.4; DB 22; Length 519; Local Similarity 74.0%; Pred. No. 1.7e-08; les 74; Conservative 0; Mismatches 26; Indels 0
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                                                                           Sequence 519 BP; 170 A; 68 C; 148 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cancer expressed polynucleotide 7520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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; 2000us-0189167.
; 2000us-0192099.
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29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
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14-MAR-2000;
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12.8%; Score 57; DB 22; Length 662; ilarity 66.9%; Pred. No. 5.4e-08; Conservative 0; Mismatches 40; Indels

Local Similarity les 81; Conserv

Best Loca Matches

Query Match

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391 GGTGAAATAAATTTCTAAGCAGCAACCATTCAAGAGGTGACTTGGGTGCTGTAAAGGC 450
327 TGTTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAA 386
                                          331 TTTTCCCCTGCCCTAGAGATTTGTGGAACTTTGAACTTGGAGAGATGATTTAGGGTATCT 390
                                                                                     387 TAAGGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAAGGC
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Pred. No. is the number of results predicted by chance to have a

Human DNA sequence from clone RPI-302D9 on chromosome 22 Contains GSSs, complete sequence.
282198 2 G1:6572207

DEFINITION

RESULT 1 HS302D9 LOCUS ACCESSION VERSION KEYWORDS SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I, Dases 1 to 145880)
Bridgeman A.
Direct Submission

REFERENCE AUTHORS TITLE

Homo sapiens. Homo sapiens

ORGANISM

AC104256 Homo sapi AC002433 Homo sapi AC027433 Homo sapi AC023112 Homo sapi AC015553 Homo sapi AL151623 Homo sapi AL157884 Human DNA D12976 Tamias asia Z82198 Human DNA s D12974 Tamias asia AB067779 Tamias si D12975 Tamias asia AB069679 Callosciu 76 Tamias asia 343 Human DNA Homo sapi Human DNA s Human DNA score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AL41943 AC062666 AC022697 AC062031 AC062031 AC018971 AC018971 AC018971 AC018971 AC018971 AC018971 AC018595 AC073840 H AL359258 H AC023471 H AC024910 ALIGNMENTS SUMMARIES TMSHP25 AB067813S3 TMSHP20A AB067779 AC027433 AC025112 AC015553 AL161623 AL157884 TMSHP27 AL441943 AC069566 AC026099 AC091987 AC062031 AC092967 AC026870 AL591842 AC002449 AC027128 AC107626 AC068063 AC073840 AL359258 AC023471 AC024910 AC022379 AC008012 AC019185 AC096992 AC117382 AC093798 AC013503 AC098595 HS302D9 DB Query Match Length 149038 162063 1385 180038 177386 137591 78.5 145880 14.2 135880 179848 161049 187640 188622 207600 158811 14451 203234 10851  $\begin{array}{c} \mathbf{G} \\ \mathbf{$ Score 63.2 63.2 63.2 63.2 62.6 62.6 62.6 61.8 61.8 õ υv 000

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                      CBIO 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert of clone RP1-302D9 The true left end of clone CTA-282F2 is at 69682 in this sequence. The true right end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elagans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22 RPI-30209 is from the library RPC-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1033. 1336. Toperat: matches 1. .299 of consensus" 1450. 1583  
/note="MIR repeat: matches 24. .160 of consensus" 1687. 1752  
/note="MIR repeat: matches 2593. .2661 of consensus" 2350. .266  
/note="AluSc repeat: matches 3. .309 of consensus" 2584. .2981  
/note="AluSc repeat: matches 2. .300 of consensus" 2584. .2981  
/note="AluSc repeat: matches 2. .300 of consensus" 3323. .334]
  Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
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/note="Ally repeat: matches 1. .309 of consensus"
3653. .3928
/note="Matches 136. .359 of consensus"
3929. .4278
/note="THELB repeat: matches 3. .364 of consensus"
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/note="L2 repeat: matches 2579. .2705 of consensus"
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1033, .1336
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//note="AALGX repeat: matches 1. :312 of consensus"
572. .759
/note="MER3 repeat: matches 1. .144 of consensus"
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note="MLT1E repeat: matches
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/db_xref="taxon:9606"
/chromosome="22"
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/clone_lib="RPCI-1"
188. .245
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JOURNAL
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                                                                                COMMENT
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/note="MLT1B repeat: matches 119. .178 of consensus" 15728. .16027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg1 repeat: matches 2. .114 of consensus"
15669. .15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 20. .137 of consensus" 12174. .12445 //note="L2 repeat: matches 1988. .2275 of consensus" 12444. .12642 //note="MIR repeat: matches 63. .241 of consensus" 13017. .13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14368. .14452

/note="MIR repeat: matches 141. .225 of consensus"

14599. .1467

/note="MIR repeat: matches 173. .262 of consensus"

1457. .15201

/note="match: GSS: Em:AQ553482"

14616. .15060
                                                                                                                                                                                             8414. .8551

hote="L2 repeat: matches 2553. .2706 of consensus 9914. .9030

/note="MIR repeat: matches 147. .262 of consensus"
                                         .302 of consensus"
                                                                                                                                 .290 of consensus"
                                                                                                                                                   7775. .8060
/note="AluJo repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Mir repeat: matches 174. .244 of consensus"
13398. .13698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14868. 15040

// Anote="MIR repeat: matches 49. .233 of consensus"

15071. .15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .99 of consensus"
repeat: matches 1. .23 of consensus"
                                                                                                                                                                                                                                                                                                            .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                        .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                              .425 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .142 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .150 of consensus"
                                                                                                                                                                                                                                                                                   9110. .9280
/note="WIR repeat: matches 91. .262 of consensus" 9283. .9412
/note="WIR repeat: matches 15. .144 of consensus" 9521. .9679
/note="FAM repeat: matches 3. .161 of consensus"
                                                                                     .77 of
                                                                                     23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 79...
10718. .11310
/note="match: GSS: Em:B14024"
10784. .11201
/note="match: GSS: Em:B43656"
11838. .11946
                       AluSx repeat: matches 1.7036
                                                                                                            7482. .7754
/note="AluJb repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSp repeat: matches 1.
13699. .13810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5071. .15188
'hote="L2 repeat: matches 2112.
15304. .15399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MLT1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:B56592"
complement(10204. .10728)
/note="match: GSS: Em:AQ701486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="match: GSS: Em:AQ225495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 76.
13806. .13919
                                                                                                                                                                                                                                                                                                                                                                                                                      9820. .10225
/note="MSTB repeat: matches 2.
complement(10179. .10678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13806. .13919
/note="MIR repeat: matches 77.
13945. .14060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: STS: Em:G49301"
13331. .13397
                                                                                       matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .10706)
                                                                                     MADE1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (10249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10383
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                     20682. .21008
/note="AluSg1 repeat: matches 1. .306 of consensus"
21239. .21553
/note="HUBRS-P3 repeat: matches 4410. .4713 of consensus"
                                                                                                                                                                                                                                                                                                     consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTACTCCAGCTTTGATG 37493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 TGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
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                          /note="MLT1B repeat: matches 178. .390 of consensus"
16546. .16854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note" "AluSp repeat: matches 1. .313 of consensus"
//note="Alusc repeat: matches 1. .299 of consensus"
16028. .16245
                                                                                                                                                                                                .4919
                                                                                                                                                                                                                                                                                                                                                                                                                                              .364 of consensus"
                                                                                                                                                                        consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23905. .23989
/note="MER66-internal repeat: matches 3017. .3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGCCCCTGTCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTTCCTTTCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAA
                                                                                                                             .4993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2417
                                                                    .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA
                                                                                                .29 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 145880;
                                                                                          /note="MSTA repeat: matches 2. .29 of conser
18324. .18392
/note="MER66-Internal repeat: matches 4919.
                                                                                                                                                                                                                                                                                   19537. .20290
/note="HERVFH21 repeat: matches 4657. .5784
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="THELB repeat: matches 1. .364 of cons
22302. .22537
/note="MER66-internal repeat: matches 2186.
                                                                                                                                                                                                /note="MER66-internal repeat: matches 4548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER66-internal repeat: matches 1210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                     2011/. .2018/
/note="131 copies 2 mer ta 68 conserved"
20513. .20666
                                                                                                                                                                                                                                                                                                                                                         /note="77 copies 2 mer tt 70 conserved"
20682. .21008
                                                                                                                                                       /note="AluJb repeat: matches 1. .311
18713. .19133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.5%; Score 351; DB 9; L. Llarity 98.6%; Pred. No. 3.8e-93; Conservative 0; Mismatches 5;
                                                                 /note="Alux repeat: matches 1.
18296. .18323
                                                                                                                                                                                                                             .19230)
Em:AQ005063'
                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ00506
19251. 19719
/note="match: GSS: Em:B14179"
19537. .20290
                                                                                                                                                                                                                             complement(18872
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23905. .239
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Matches
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RESULT 2 TMSHP20A

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   ROD 03-FEB-1999
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Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hyglenic
Sciences, Kitasato University, Laboratory of Molecular Biology;
11-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
Fax:0427-78-9403)
                                                                                                                                Euteleostomi;
1e; Sciurinae;
                                                                 plasma
                                                                                                                                                                                                               with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 AAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAAGGAGGCCATG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAAAATGCCCCTGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCTCTTCCTTTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCAT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 CATGTAGAAGTTGCTGGACCTCCAGCACACCCCCAGGCCCCCAGAAGAAGTGGGGCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 GAGCCTGTGGTCTTCACAGAGGTCCTGTACAATACCCAGAGGGACTTGAAGGAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D12974.1 G1:287467
HP-20; collagen-like domain; hibernation-related protein;
                                                                                                                                                                                             and Shiba,T.
plasma proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                Craniata; Vertebrata; Eut
Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at nt 161-277"
                                                                               protein.
Tamias asiaticus liver cDNA to mRNA, clone:pCM20-7.
Tamias sibiricus
   linear
                  complete cds.
                                                                                                                                                                                           Takamatsu, N., Ohba, K., Kondo, J., Kondo, N. and
Hibernation-associated gene regulation of plas
collagen-like domain in mammalian hibernators
Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
93180798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7.3e-34;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 CATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAAT 377
   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Tamias sibiricus"
/db_xref="taxon:64680"
/clone="pCM20-7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="collagen-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 151.2;
Pred. No. 7.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA02351.1"
/db_xref="GI:287468"
 TMSHP20A 1265 bp Tamias asiaticus mRNA for HP-20,
                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver"
89. .679
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="HP-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="HP-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1238. .1243
1265
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67.8%;
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                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity 67.8
Matches 229; Conservative
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158. .67
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polyA_site
BASE COUNT 35.
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/translation="MPAQRGGALSMGAAGFWILVLSITSALADSNNGGNSEPCGPPGP
PGPPGIPGFGGARGALGPPGPPGPTGPGQGPGDVERCSSRRKSAFAVKLSERPPE
PPCPTVFKEALYNDGFHRMATGFSCVLPGVYNGFDIRLFQSSVKIRLMRDGIQVR
EKEAQANDSYKHAMGSVIMALGKGDKVWLESKLKGTESEKGITHIVFFGYLLYGK"
                                                                                                                                                                                         03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-ANG-1992) Nobubiko Takamatsu, School of Hygienic
Sciences, Kitasato University, Laboratory of Molecular Biology;
1-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408)
                                                                                                                                                                                                                                                                                                                      Tamias sibiricus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                         TMSHP25 2005 bp mRNA linear ROD 03-FEB-1 Tamias asiaticus mRNA for HP-25, complete cds. D12975 1 GI:287469 HP-25; collagen-like domain; hibernation-related protein; plasma protein.
Takamatsu, N., Obba, K., Kondo, J., Kondo, N. and Shiba, T. Hibernation-associated gene regulation of plasma proteins with collagen-like domain in mammalian hibernators Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AGGACCTCCAGGCATCCCAGGCTTTCCAGGCGCTCCTGGAGCACTTGGTCCACCAGGACC 307
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                                                                                                                                                                                                                                                                                                  Tamias asiaticus liver cDNA to mRNA, clone:pCM25-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="collagen-like domain at nt 231-356"
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Pred. No. 5.1e-14;
0; Mismatches 159;
                                                                          /organism="Tamias sibiricus"
/db_xref="taxon:64680"
/clone="pcM25-3"
/tissue_type="liver"
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                                                          CATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAAT
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/protein_id="BAA02352.1"
/db_xref="G1:287470"
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Location/Qualifiers
1. .2005
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/product="HP-25"
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54.4%;
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Takamatsu, N.
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Best Local Similarity 54.4
Matches 193; Conservative
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RQGPGAAGREDDGPKGPSVKDPCRRSAFTVKSGRLPPPSEPVVFTEVLYNYQRDL

RASTGVFRUVEPGNYFFSFDVELYHCKVKIGLMKNHIQVMEKHQLSKNEYENASGAMI

MPLRQGDKVWLEADVETEEPDQAKVVIYFSGFLISS"

MPLRQGDKVWLEADVETEEPDQAKVVIYFSGFLISS"

2573. .2710

/gene="HP-20"

968. .5000
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                                                                                                               ROD 26-OCT-2001
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                      Shiba, T.
                                                                                                                                                                                                                                                                                                                    Ono,M., Hosoe,Y., Azuma,S., Shoji,M., Nara,K., Kondo,N., Shiba,T and Takamatsu,N.
HNF-I regulates the liver-specific transcription of the chipmunk HP-20 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAGGAGGCCATG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-A0G-2001) Motoharu Ono, Kitasato University, Department of Biosciences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail.ms99805m@stu.sci.kitasato-u.ac.jp, Tel:81427789408, Fax:81427789408)
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                                                                                                               linear
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Tamias sibiricus gene for HP-20, complete cds.
AB067779
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1518. 1684
10in(1678. 1684,2573. .2710,3968.
10in(1678. 1684,2573. .2710,3968.
/gene="HP-20"
/codon_start=1
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Tamias sibiricus DNA, clone:lamdaCM20G1
Tamias sibiricus
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/Organism="Tamias sibiricus"
/Ob_xref="taxon:64680"
/clone="lamdacM20G1"
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/db_xref="GI:15706342"
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1018 c
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152 GGGTCCTTCCAGCCCATCATATTCAAGGAGTCTCTGTACAACCGGGAGGACCACTATAAC 211
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-AUG-2001) Nobuhiko Takamatsu, Kitasato University, Department of Blosciences, School of Science; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:takamatu@jet.sci.kitasato-u.ac.jp, Tel:81427789408,
                                                                                     151 TGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTCCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 CTTCCTTTCAAGCCCATCATCTTCACAGGGTCCTGTACAATGCCCAGAGGGATTTAAAG 270
                          282 AGICTITGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
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/gene="HP-25"
                                                                                                                                                                                                                                                  Callosciurus caniceps HP-25 pseudogene, exon 3, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1658, AB069678.1:26. .185,39.
            GCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTTAAAGGAGGCCATGGG
                                                                                                                               342 TIGCAAGGIGAATATIIGGCTAAIGAGGAAGCAAAITIIGGCTAATAAGGAAGAA 396
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Callosciurus caniceps
                                                                                                                                                                                                                                                                                                                                                                                                                   Kojima,M., Shiba,T., Kondo,N. and Takamatsu,N.
The tree squirrel HP-25 gene is a pseudogene
Eur. J. Biochem. 268 (22), 5997-6002 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Callosciurus caniceps"
/db_xref="taxon.64664"
/clone="lambda T82561"
join(AB06/813.1:1503. .1658,AB0690/
/gene="HP-25"
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Pred. No. 2.6e-09;
0; Mismatches 119;
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39. .>559
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AB069679.1 GI:18149913
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Takamatsu, N.
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Laborated (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, Cabonitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clonerquest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gl:3164067.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/HGP/Chr22 RP1-302D9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                HS302D9 145880 bp DNA linear PRI 12-DEC-1999
Human DNA sequence from clone RPI-302D9 on chromosome 22 Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         271 GAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 GGACTGTTTCAGAGTTCTGTGAAGATAAGTCTCATGAGGAA 312
                                                                                                                                                            331 GAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAA 371
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/organism="Homo sapiens"
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/note~"MER3 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSs, complete sequence.
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1 (bases 1 to 145880)
Bridgeman, A.
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// Inde="Alusp repeat: matches 1299 of consensus" // Inde="Alusp repeat: matches 24160 of consensus" // Inde="Alusp repeat: matches 24160 of consensus" // Inde="L2 repeat: matches 25932661 of consensus" // Inde="Alusc repeat: matches 3309 of consensus" // Inde="Alusq repeat: matches 2300 of consensus" // Inde="Alusq repeat: matches 2300 of consensus"	33233343 //note="MLTIE repeat: matches 116136 of consensus" //note="AluY repeat: matches 1309 of consensus" //note="MLTIE repeat: matches 136359 of consensus" //note="MLTIE repeat: matches 3364 of consensus" //note="MLTIE repeat: matches 3364 of consensus" //note="MLTIE repeat: matches 359568 of consensus" //note="MLTIE repeat: matches 359568 of consensus" //note="MLTIE repeat: matches 359568 of consensus" //note="12" /	repeat: matches 1311 of consensus repeat: matches 1311 of consensus repeat: matches 123 of consensus repeat: matches 1302 of consensus repeat: matches 2377 of consensus repeat: matches 9290 of consensus repeat: matches 1295 of consensus repeat: matches 1295 of consensus	### Miles
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/note="match: GSS: Em:AQ005063"
/19251. .19719
/note="match: GSS: Em:B14179"
19537. .20290
/note="HERYFH21 repeat: matches 4657. .5784 of consensus"
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18324. .18392
/note="MER66-internal repeat: matches 4919. .4993 of
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/note="AluJb repeat: matches 1. .311 of consensus"
18713. .1913
/note="MER66-internal repeat: matches 4548. .4919 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           consensus"
23905. .23989
/note="MER66-internal repeat: matches 3017. .3102 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                15490. .1562

/note="AluSg1 repeat: matches 2. .114 of consensus"

1569. .15727

/note="MLT1B repeat: matches 119. .178 of consensus"

15728. .16027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1B repeat: matches 178. .390 of consensus"
16546. 16854
/note="Alux repeat: matches 1. .300 of consensus"
18296. 18323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="THEIB repeat: matches 1. .364 of consensus" 22302. .22537
/note="MER66-internal repeat: matches 2186. .2417 of
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14868. 15040
/note="MIR repeat: matches 49. .233 of consensus"
15071. .15188
/note="L2 repeat: matches 2112. .2239 of consensus"
15304. .1539
/note="MITIB repeat: matches 1. .99 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Alusc repeat: matches 1. .299 of consensus"
16028. .16245
                                                                                                                                                                     /note="MIR repeat: matches 141. .225 of consensus"
14589. .14679
                                                                                                                                                                                                               /note="MIR repeat: matches 173. .262 of consensus"
14597. .15201
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/note="MIR repeat: matches 76. .174 of consensus" 13806. .13919
/note="MIR repeat: matches 77. .189 of consensus" 13945. .14060
                                                                               /note="MIR repeat: matches 24. .142 of consensus" 14061. .14367
/note="Alux repeat: matches 1. .301 of consensus" 14368. .14452
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14616. .15060
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171 AAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAACTTCCTCTTCCTTTCAAGCCCATCAT 230

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4364. 4569
//octe="Lo repeat: matches 2535. 2750 of consensus"
4612. 4934
//octe="AluJo repeat: matches 1. 307 of consensus"
4934. 5220
//octe="AluJo repeat: matches 1. .287 of consensus"
5221. 5268
//octe="16 copies 3 mer taa 97 conserved"
complement(5266. 5727)
//octe="match: GSS: Em:AQ028870"
//octe="match: GSS: Em:AQ028870"
//octe=match: GSS: Em:AQ057814"
                                                                                                                                                                                                                                             3670. .3742
/note="MRR82 repeat: matches 580. .653 of consensus"
3763. .4128
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      'note="AluJb repeat: matches 1. .126 of consensus"
                                                                                                                                                                                                                                                                                                                           .386 of consensus"
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27067. .27138
                                                                                                                                                              3418. .3477
/note="30 copies 2 mer ac 90 conserved"
3423. .3478
/note="14 copies 4 mer caca 94 conserved"
3670. .3742
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                                             1374. 1869 revers 3548.
/note="LiP repeat: matches 3221.
1952. 2076
                        758. 1385
/note="LIP_repeat: matches 3548.
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//note="MIR repeat: matches 22. ...

10322. 16495

//note="LiPA2 repeat: matches 7.

16265. 16787
                                                                                                                                                                                                                                                                                        repeat: matches 1.
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/note-match: GSS: Em:AQ559531"
4364, 4569
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21369. 21551
/note="MIR repeat: matches 2.
22494. 22697
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20811. .21058
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During Sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep CTA-73284 is from the human BAC library described in U-J. Kim et al. (1996)
                                                                                                                                                                                                                                                                                                                                                            HS732E4 90497 bp DNA linear PRI.12-DEC-1999 Human DNA sequence from clone CTA-732E4 on chromosome 22q12.1 Contains ESTs, STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of clone CTA-732E4 The true left end of clone RP11-54116 is at 5510 in this sequence. The true right end of clone CTA-544A11 is at 41939 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone is 200 Jul 8, 1999 this sequence version replaced gi:5304865. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats. but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90497)
90879 AAGATCTGCATTTGTGGTGAAACTGATCGGACCCCTCCCAGTGCCCTTCTAGCCCATTGT 90820
                                                                                                     90760
                                                                                                                                                              350
                                                             290
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632. .757
                                                                                    90819 CTTCAAGGAAGCCCTTTATAAATACTCAGTTCCATTTCCATTTCTCTGGTGAAGGATTCAC
                                                                                                                                        291 TTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATCATTGCAAGGT
                                                           CTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAAAAGGAGGCCATGGGAGTCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT978SK-A2"
2. .631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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/clone="CTA-732E4"
                                                                                                                                                                                                                                             Db 90699 AAATGTGGGTATTATGAGGAA 90679
                                                                                                                                                                                                                    GAATATTTGGCTAATGAGGAA 371
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AL008722.16 GI:5419644
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TITLE
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40551. 40904
/note="FHELB repeat: matches 3. 364 of consensus"
40905. 41859
/note="TigGER1 repeat: matches 1394. .2418 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(41368 ... account tepeat. marchies 1394. .. 2418 OI Consensus" complement(41368 ... account (41368 ... account (41368 ... account (41368 ... account (41362 ... account (4136
                                                                                                                                                                                                                                                                                                        .4984 of consensus"
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/note="THELB repeat: matches 3. .364 of consensus" 38938. .40548
/note="THELB-INTERNAL repeat: matches 1. .1580 of
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49916. .50351
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/note="AluSg1 repeat: matches 1. .293 of consensus"
48399. .48549
                               .2744 of consensus'
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/note="55 copies 2 mer ag 67 conserved"
47276. 47434
/47016="MRESA repeat: matches 4. .189 of consensus"
47698. 47991
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                                                                                                                                                /note="match: GSS: Em:AQ805065"
50076. .50449
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28759, .28798
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Chases I to 135880)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Chang, J., Changaro, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Choepel, Y., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

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Ginde, S., Gord, S., Goyette, M., Graham, L., Gardorne, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Gardorne, R.,

Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

Macathy, M., McEwan, P., McKernan, K., McPheeters, R., Meltiews, C.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Ribey, R., Klse, C., Rogov, P.,

Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,

Strauss, N., Subramanian, A., Travis, N., Trigilio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Direct, Submission, C., Limmer, A., and Scoty, M.,

Direct, Submission, C., Chimer, A., and Scoty, M.,

Condon, C., Chimer, A., and Scoty, M.,

Condon, C., Chimer, A., and Scoty, M.,

Condon, C., Chimer, C., Chimer, C.
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Direct Summission

Eneman, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Chopeel, Y., Collymore, A.,

Cook, A., Cooke, P., Parcellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

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Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,

Mcarthy, M., Meldrim, J., Macdonald, P., Major, J., Matthews, C.,

Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,

O'Connor, T., O'Donnell, P., O'Neil, D., O'Ilver, J., Peterson, K.,

Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,

Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J.,

Tesfaye, S., Theodore, J., Topham, K., Travers, W., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zaihoun, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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Length 90497;
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Homo sapiens chromosome 8 clone CTD-2384G12 map 8,
IN PROGRESS ***, 1 ordered piece.
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Homo sapiens chromosome 8, clone CTD-2384G12
Unpublished
Score 63.4; DB 9;
Pred. No. 1.4e-07;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                      39321 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 39357
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    14.28;
                                                                                    Conservative
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Query Match
Best Local Similarity
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Homo sapiens genomic DNA
2 (bases 1 to 51000)
2 (bases 1 to 51000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Bulnet Submission
Submitted (24-MAY-2002) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP005265 51000 bp DNA linear PRI 07-JUN-2002 Homo sapiens genomic DNA, chromosome 18, clone:RP11-78F17, complete
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                                    Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2002 this sequence version replaced gi:21699681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 135880: contig of 135880 bp in length.
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                                                                                                All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L22077
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Pred. No. 1.5e-07;
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/clone_lib="CITD1 Human BAC"
42430 a 25457 c 25972 g 42021 t
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/db_xref="taxon:9606"
/chromosome="8"
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Zembek, L., Zimmer, A. and Zody, M.
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AP005265.2 GI:21328206
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                     Direct Submission
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suethiro-chou, Tsurumi.ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@ges.riken.go.jp, WIL:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-445-503-9170) on Jun 6, 2002 this sequence version replaced gi:21218138.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens chromosome 18, clone RP11-78F17
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Pred. No. 1.6e-07;
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9626 c 9391 g 17873 t
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1. 51000
/organism="Homo sapiens"
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/chromosome="18"
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AC027433.2 GI:7677878
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L Similarity 74.1%;
80; Conservative
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97.159

97.150; gap of 100 bp

10.2801 10.2801; contig of 5541 bp in length

10.2802 10.2901; gap of 100 bp

10.2902 10.8682; contig of 5781 bp in length

10.8683 10.8782; gap of 100 bp

115.195 115.294; gap of 100 bp

115.295 12.3411; contig of 8117 bp in length

115.3512 12.3511; gap of 100 bp

12.3412 12.3511; gap of 100 bp

12.3512 13.2644; gap of 100 bp

13.2645 13.2744; gap of 100 bp

13.2745 13.2744; gap of 100 bp

13.2745 13.2744; gap of 100 bp

13.2745 13.2744; gap of 100 bp
.00 bp
5003 bp in length
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87792: contig of 5121 bp in length
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92294: contig of 4402 bp in length
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1. .1689
                                                       69197: gap of 100 bp 73278: contig of 4081 bp
                                                                                                                                                                    29: gap of 100 bp
82571: contig of 4742 bp
                                                                                                         73378: gap of 100 bp
77729: contig of 4351 bp
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28100. 31388
/note="assembly_fragment"
31489. 34192
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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43796. .48598
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'note="assembly_fragment"
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/note="assembly_fragment"
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14661. .17033
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment
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/db_xref="taxon:9606"
/chromosome="18"
194: gap of 1
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...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                   Center project name: L782.

Center clone name: 78_F17

Center clone name: 78_F17

Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap: version 0.960731

Consensus quality: 124489 bases at least Q40

Consensus quality: 133382 bases at least Q30

Consensus quality: 137772 bases at least Q20

Insert size: 139000; agarose-fp

Insert size: 141014; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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188: gap of 100 bp
34192: contig
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21078: contig of 2231 bp in length
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7: contig of 3869 bp in length
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55272: contig of 2605 bp in length
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59485: contig of 4113 bp in length
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63994: contig of 4409 bp in length
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Web site: http://www-seq.wi.mit.edu
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 6, clone RP11-608N7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 8, 2000 this sequence version replaced gi:7158923. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACO25112 149038 bp DNA linear HTG 08-APR-;
Homo sapiens chromosome 6 clone RP11-608N7 map 6, WORKING DRAFT
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Center: Whitehead Institute/ MIT Center for Genome Research
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14.1%; Score 63.2; DB 2;
Best Local Similarity 74.1%; Pred. No. 1.7e-07;
Matches 80; Conservative 0; Mismatches 28;
              48699. .52567
/note="assembly_fragment"
52668. .55272
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/note="assembly_fragment"
59586. .63994
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                 Sequencing vector: M13: M77815; 100% of reads Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator B1g Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 132985 bases at least Q40 Consensus quality: 140748 bases at least Q30 Consensus quality: 140748 bases at least Q20 Insert size: 138000; agarose-fp Insert size: 138000; agarose-fp Quality coverage: 3.6 in Q20 bases; sum-of-contigs Quality coverage: 3.6 in Q20 bases; sum-of-contigs
102457; gap of 100 bp 112952; contig of 10495 bp in length 113052; qap of 100 bp
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102357: contig of 10275 bp in length
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45639: contig of 4775 bp in length
739: gap of 100 bp
50826: contig of 5087 bp in length
26: gap of 100 bp
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4814: contig of 1378 bp in length
4914: gap of 100 bp
6853: contig of 1939 bp in length
6953: gap of 100 bp
9114: contig of 2161 bp in length
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71321: contig of 7815 bp in length
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14633: contig of 2462 bp in length
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                                                                              Center clone name: 608_N_
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113053 124237: contig of 11185 bp in length 124238 124337: gap of 100 bp 124338 135694: contig of 11357 bp in length 135595 135794: gap of 100 bp 135795 149038: contig of 13244 bp in length.
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135795. .149038
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266. .1355
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 162063)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Batheria,J., Bantcoh,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Burbaria,J., Bantcoh,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Burbaria,J., Bantcoh,J., Blanker,T., Chraitstopoulos,C., Clevaland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davida,N., Davis,C., ChowdhryI.T., Christopoulos,C., Clevaland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., ChowdhryI.T., Christopoulos,C., Clevaland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Carroll,T., Daderich,D.A., Delaney,K.R., Delaney,C., Elhaj,C., Esoctto,M., Falls,T., Perraguto,D., Flagar,D., Edwards,C.C., Elhaj,C., Esoctto,M., Falls,R., Garcia,A., Garrer,T., Garis,L., Dinny,Y., Garis,J.M., Gao,J., Garcia,A., Garrer,T., Garis,R., Garis,R., Hamilton,K.J., Harris,C., Harris
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Direct Submission
Submitted (17-NOV-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                     340 CATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATT 399
                                                           Gaps
                                                        ;
Length 149038;
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Score 63.2; DB 2;
Pred. No. 1.7e-07;
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Unpublished
2 (bases 1 to 162063)
14.1%;
74.1%;
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                          Best_Local Similarity
Matches 80; Conserv
  Query Match
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COMMENT

REFERENCE AUTHORS TITLE JOURNAL

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ccagcaataa (a)caagtagaat
gctgaattg (t)tcttatttt
catctaggtg(c)tggttccatg
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Phrap Value Range
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Pred. No. 2.6e-07;
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832. .2859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-100N10"
706. .734
/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="L1MA4"
4109. .4207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L1MA4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family-"Aluy"
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79.6%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                   Direct Submission
Submitted (30-MAR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                             Direct Submission
Submitted (12-0101.2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STSs are identified using ePCR (Genome Res. 7:541-550) searches a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-JUL-2001) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                 of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Mar 30, 2001 Lhis sequence version replaced gi:13487890.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
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acccacctta(g)cctcccaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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0.00234308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40:
  TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cacccacctt(t)acctcccaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus changing edits: N's in consensus :
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  lor Plaza, Houston,
(bases 1 to 162063)
                                                                                                                                                               (bases 1 to 162063)
                                                                                                                                                                                                                                                                                                            (bases 1 to 162063)
                                                                                                                                                                                                                                                                                                                                                          Submission
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p of 100 bp contig of 4450 bp in length

bp in length

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97529 97628: gap of 110 bp 110 bp 110521 101520: contig of 3892 bp in length 101521 101520: contig of 3892 bp in length 101521 112966: contig of 11346 bp in length 112967 113066: gap of 100 bp 113067 119217: contig of 6151 bp in length 119218 119317: gap of 100 bp 119318 121556: contig of 2239 bp in length 11257 121656: gap of 100 bp 121557 134400: contig of 12744 bp in length 134501 134500: gap of 100 bp 134501 134500: gap of 100 bp 134501 134501 ap of 100 bp 144935 145034: contig of 13784 bp in length 145035 146818: contig of 3784 bp in length 145035 146818: contig of 3784 bp in length
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/note="assembly_fragment:00194
fragment_chain:1"
25996. .31543
/note="assembly_fragment:00852
fragment_chain:2"
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//note=assembly_fragment:00602
fragment_chain:2"
39349 ..49948
//note=assembly_fragment:01593
fragment_chain:3"
50049 ..66131
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/note=assembly_fragment:01966
fragment_chain:3"
66232 . .80131
/note=assembly_fragment:02033
fragment_chain:4"
80232 . .89785
/note=assembly_fragment:00372
fragment_chain:4"
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113067...19217
/note="assembly_fragment:01397"
119318...121556
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/note="assembly_fragment:01568"
134501. 144934
/note="assembly_fragment:01617"
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fragment_chain:1"
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note="assembly_fragment:02305
ragment_chain:5"
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/note="assembly_fragment:00011
fragment_chain:5"
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101621. .112966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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1. .3511
                          92978: contiq of
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       gap of
                                               gap of
                                                                    97528:
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                                                                                                                                                                                                                                                          175134 bp DNA linear HTG 10-JUL-2001
HOMO sapiens chromosome 9 clone RP11-1K21, *** SEQUENCING IN
PROGRESS ***, 20 unordered pieces.
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0
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Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 24% of reads
Consensus quality: 164370 bases at least Q40
Consensus quality: 168213 bases at least Q30
Consensus quality: 10527 bases at least Q30
Consensus quality: 170527 bases at least Q30
Insert size: 17324; sum-of-contigs
Insert size: 188172; 4.4% error; agarose-fp
Quality coverage: 4.13 in Q20 bases; sum-of-contigs Quality
coverage: 4.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175134)
Mclay,K.
                                                                    29373 ACTTTGAACTTGAGAGAGATGATTTAGGGTATGCCAGAAGAATTTCTAAGCAGCAAAGC 29314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                        355 ATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCAAAGC 414
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Aug 27, 2000 this sequence version replaced gi:9863606.
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19; Indels
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3512 3611: gap of 100 bp
3612 25895: contig of 22284 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143: gap of 100 bp 39248: contig of 7605 bp in length 148: gap of 100 bp in length 149348: contig of 10600 bp in length 148: gap of 100 bp
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80131: contig of 13900 bp in length
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                                                                                                                                                            Db 29313 ATTCAAGAGGTGACTTGGGTGCTGTTAAAGACA 29281
  Mismatches
                                                                                                                                    415 ATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCA 447
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74;
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SOURCE

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Takamatsu, N.
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Submitted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Callo 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Jul 29, 2001 this sequence version replaced gi:15026899.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the Geature table with their source databases: Em:, EMBL; Sw:, SWISSROR! Tr:, TERMBL; Wp:, WORMPEP! Information on the WORMPEP database can be found at his proposal content of the worm 
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RPI1-462B18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83975 ACTTTGAACTTGAGAGAGATGATTTAGGGTATGCAGAAGAAATTTCTAAGCAGCAAGC 83916
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                                                                             /note="assembly_fragment:01972"
15279. 165020
/note="assembly_fragment:00951
fragment_chain:6"
165121. 175134
/note="assembly_fragment:01119
fragment_chain:6
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.6; DB 2;
Pred. No. 2.7e-07;
                          /note="assembly_fragment:01696"
148919. .152178
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36761 c 35231 g 49719 t
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http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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.148818
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Whitehead, S.
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79.68;
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QCPPGMRGPPGTPGKPGPPGMNGFPGLPGPPGPPGMTVNCHSKGTSAFAVKANELPPA PSQPVIFKEALHDAQGHFDLATGVFTCPVPGLYQFGFHIEAVQRAVKVSLMRNGTQVM EREAEAQDGYEHISGTAILQLGMEDRVWLENKLSQTDLERGTVQAVFSGFLIHEN"
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Submitted (21-AUG-1992) Nobuhiko Takamatsu, School of Hyglenic
Sciences, Kitasato University, Laboratory of Molecular Biology;
11-15-1 Kitasato, Sagamihara, Kanagawa 228, Japan (Tel:0427-78-9408,
Fax:0427-78-9403)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
This sequence is the entire insert of clone RP11-462B18 The true right end of clone RP11-555J4 is at 30638 in this sequence. The true right end of clone RP11-1K21 is at 97783 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takamatsu. N., Obba. K., Kondo, J., Kondo, N. and Shiba, T.
Hibernation-associated gene regulation of plasma proteins with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D12976.1 GI:287471
HP-27; collagen-like domain; hibernation-related protein; plasma
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Tamias asiaticus liver cDNA to mRNA, clone:pCM27-3.
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Mol. Cell. Biol. 13 (3), 1516-1521 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.6; DB 9;
Pred. No. 2.7e-07;
0; Mismatches 19;
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/db_xref="G1:287472"
                                                                                                                                         /organism="Homo sapiens"
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/clone="pCM27-3"
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76326. .77014
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/clone="RP11-462B18"
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79.6%;
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                                          Query Match
Best Local Similarity 55.6%; Pred. No. 2e-07;
Matches 120; Conservative 0; Mismatches 96; Indels 0;
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155. .709
/product="HP-27"
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Search completed: February 20, 2003, 05:05:34 Job time : 2438.16 secs

Scoring table:

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Database

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BES80165 Kq37h09.y
BQ939199 ACENCOURT
AL3430B Terracodon
AL311965 Terracodon
BES1564 Kq47e0B.y
ANG75997 SWPD25CAU
AN179710 SWPD25CAU
AN179710 SWPD25CAU
AN179745 SWPD25CAU
BE758489 SWPACALL1
AN179745 SWPD25CAU
AN470940 SWPD25CAU
AN470940 SWPD25CAU
AN470940 SWPD25CAU
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BE285930 601097647
AN17949 SWPD25CAU
BE285930 601097647
AN17949 SWPD25CAU
BE285930 601097647
AN17945 SWPD25CAU
                                                                                                                                                                                                                                          BE581944 kq56q01.7
BE579460 kq28b07.9
BE579541 kq29d06.7
BE579571 kq25a09.7
BE579572 kq29h04.7
BJ136441 BJ136441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244751 342 bp mRNA linear EST 14-NOV-1994 HSC28C121 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                      BE581103 kq42c06.y
BE579707 kq30f11.y
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B1742399 kt38903 y
B0335482 PM4 +MT043
B1323796 kt74h07 y
BESF9244 kq24e08 y
BG310518 SWOY3MCAM
BE383449 6012974448
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes, M. D., Duprat,S., Houlgatte,R., Joneau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                              BJ136441
BJ108893
BJ002073
BI323061
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 31604728698
Email: genexpress@genethon.fr
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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AW179710
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BE758489
AW179745
AW409404
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AW874708
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BE579572
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244751
244751.1 GI:573911
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AUTHORS
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BE121287 UI-R-CA0-
BI863711 Kx47e02.y
AI617644 zehn1908.
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                                                                   February 19, 2003, 23:48:42; Search time 391.859 Seconds (without alignments) 6406.126 Million cell updates/sec
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        5.1.3
Compugen Ltd.
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                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
         GenCore version
Copyright (c) 1993 - 2003
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                                                 - nucleic search, using sw model
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AU205784
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Listing first 45 s
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Score

Result Š.

kt38903.y PM4-MT043

kt68h01.y

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BASE COUNT
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BI322379
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KEYWORDS
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                                                                                                                                                                                /tissue_type="total brain"
/dev.stage="3 months old"
/dev.stage="3 months old"
/dev.stage="3 months old"
/dev.stage="1" HindIII;
/site_2: NotI; sex=Female; dev.stage=3 months old;
/site_2: NotI; sex=Female; dev.stage=3 months old;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=musNa was oligo-(dr) primed and directionally
/cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
// Soares, P.N.A.S in press" 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazaa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
1. (bases 1 to 638)
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 CCGTCCGACTGTCCTCGCCGGTTGGTCAGTGTGAATTTGTGACAGCTGCAGTTGCTCCC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 GCCCCCGAGCAGCAGCGAGGAGTCTACCGTGGCTCCNGANTTTCCCAAAAATTCAGCAGAA 167
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-28c12
Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 CCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU205784 anpublished oligo-capped cDNA library, stage Ll
Caenorhabditis elegans cDNA clone yk855b02 5', mRNA sequence.
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0
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                                                                                                                                              /clone_lib="normalized infant brain cDNA"
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Contact: Yuji Kohara
Contact: Yuji Kohara
Conne Biology Lab.
National Institute of Genetics
Yata Illi, Mashima, Shizuoka 411, Japan
Fax: 81-559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.6;
Pred. No. 1;
                                                                                  /organism="Homo sapiens"
                                                                                                   /db_xref="taxon:9606"
/clone="c-28c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="N2"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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AU205784.1 GI:14838413
                                                                                                                                                                   /sex="Female"
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ilarity 55.1%;
Conservative
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Best Local Simi
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Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dante, M. Marra, M., Hillier, L., Rucaba, T., Theising, B., Bowers, Y., Glifton, S., Chiapelli, B., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M., Hillier, L., Rucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tasgareishvilli, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
/dev_stage="Ll"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kx20d10.y3 Parastrongyloides trichosuri FL pAMF1 v1 Chiapelli
McCarter Parastrongyloides trichosuri cDNA 5' similar to TR:Q61436
Q61436 PROCOLLAGEN, TYPE IV, ALPHA 5 ;contains element PTR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                             563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 AGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGA 140
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Parastrongyloides trichosuri FL pAMP1
Chiapelli McCarter"
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Parastrongyloides trichosuri
Eukaryota; Metazoa; Nemacoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
                                                                                                                                                                                                                                                                        Length 638;
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/db_xref="taxon:131310"
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The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
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                                                                                                                                                                                                                                                                  Score 39.4; DB 9;
Pred. No. 1.2;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                 193
                                                                                                                                                                                                                                                                                                                              73;
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                                                                                                                                                                                                                                                                                                      Local
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/strain="sprague Dawley"
/db_xref="taxon:10116"
/clone="U1-R-CA0-baw-b-08-0-U1"
/clone="Lib="U1-R-CA0"
/lab_host="DH108 (Life Technologies)"
/lab_host="Life"
/lab_host="Lib="Lib="Lib"
/lab_host="Lib"

James McCarter at Washington University, St. Louis. The CDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Warwick Grant of AgRearch, New Zealand 103 c 123 g 100 t.
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UI-R-CAO-baw-b-08-0-UI.sl UI-R-CAO Rattus norvegicus cDNA clone
UI-R-CAO-baw-b-08-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 531)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 AGGAAAAGATGGATTACCAGGATTCCCAGGAATTAAAGGAGAAAGTGGTTTCCCTGGAGC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 AGAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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Pred. No. 1.9;
0; Mismatches
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BE121287.1 GI:8513392
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Best Local Similarity 61.4%;
Matches 62; Conservative
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kx47e02.y1 Parastrongyloides trichosuri FL pAMP1 v1 Chiapelli McCarter Parastrongyloides trichosuri CDNA 5' similar to SW:cA34_ASCSU P27393 COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR. [1] scontains element PTR5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa: Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
1 (bases 1 to 552)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
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     derived, please visit our web u. The subtraction has been
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Seq primer: -40RP from Gibco High quality sequence stop: 395.
                                                   Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                  526 CTTCTTGCCCTCACAGGACAGTCAGGGCTCCCTGGCCTCCCTGGACAGCAGGGGGACTCCT 467
                                                                                                                                                                                                                                                                                                              Gaps
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                             DB 10; Length 531;
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/db_xref="taxon:131310"
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from which this clone was derived, site at ratest.eng.uiowa.edu. The previously described in (Bonaldo, Genome Research 6:791-806, 1996)
                                                                                                                                                                               145 t
                                                                                                                                                                                                                                                                                   Pred. No. 1.9;
0; Mismatches
                                                                                           TAG_LIB=UI-R-CAO
TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"
                                                                                                                                                                                                                                                                Score 38.6;
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/lab_host="DH10B"
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Parastrongyloides trichosuri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Warwick Grant of AgRearch, New Zealand (Warwick, grantgaresch.co.nz)."
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
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ner. EcoRI
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Zehn1908.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
CDNA 5', mRNA sequence.
AI617644
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                                                                                                                                                                                                                        45 AGAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGC 104
                                                                                                                                                                Gaps
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/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrF'"
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                                                                                                                          24.9%; Score 38.6; DB 13; Length 552; 61.4%; Pred. No. 1.9;
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PORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                      105 ACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGA 145
                                                                                                                                                                                                                                                                                         103 ACCAGGTATGCCAGGATTGAAAGGAGAATTAGAGAATTTA 343
                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Liew CC Brigham and Women's Hospital Harvard Medical School TS Francis St. Boston, MA 02115, USA Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 t
                                                                                                                                                              0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
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/organism="Danio rerio"
/db_xref="taxon:7955"
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109 c 1
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AI617644
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BJ121588 unpublished oligo-capped cDNA library, C. elegans Ll stage Caenorhabditis elegans cDNA clone ykl278c03 5', mRNA sequence.
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//sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into ppc86" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE580165 468 bp mRNA linear EST 09-MAY-2001 kq37h09.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to TR: P79758 P79758 COLLAGEN ; contains TAR1.t3 TAR1 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 770)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
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/strain="N2"
/db_xref="laxon:6239"
/clone="yx1278c03"
/clone="unpublished oligo-capped cDNA library,
elegans L1 stage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accomplementary view of the C.elegans genome Unpublished (2002)
Contact: Tadabau Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mashima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
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24.4%; Score 37.8; Dl
55.8%; Pred. No. 3.2;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ121588.1 GI:18281723
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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61.5%;
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                                                                                           Unpublished (1999)
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CNS05LPT/c
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/Jab_host="XL-IBLUE MRF" (Stratagene); Site_1:
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
ECORI; Site_2: Xhof; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. CDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the ECORI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700).

(range, 100-1700).
                                                                                                                                                                     McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvilli, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ939199 889 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8922132 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6395968 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@hih.gov). DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. High quality sequence stop: 325.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: McCarter JP
Contact: McCarter JP
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1800
Fax: 314 286 1800

    468 "Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"

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                                                                                                        Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Panagrolaimoidea, Strongyloididae, Strongyloides.
1 (bases 1 to 468)
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/clone_lib="TBN95TM-SSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                  Strongyloides stercoralis
                                                                                           stercoralis
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BQ939199.1 GI:22354677
    BE580165
BE580165.1 GI:9831107
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nes 68; Conservative
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/clone="IMAGE:6395968"
/clone="IMAGE:6395968"
/clone="InhaGE:6395968"
/lab_host="broil graph=cresistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="organization organization organizat
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Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
Tetraodontidae; Tetraodontidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
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1 (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
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Location/Qualifiers
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Query Match
Best Local Similarity
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                                                   Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Location/Qualifiers
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Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Tetracdontidae; Tetracdon.

1 (bases 1 to 1101)

1 (bases 1 to 1101)

1 (bases 1 to 1101)

Bernot, A., Fizames, C., Wincker, P., Bouneau, L., Fisher, C., Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                            /note="Genoscope sequence ID : C0AA048AB04C1-end : T7" 182\ c 179\ g 136\ t 47\ others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 GTGGGAGTTCCTGGACCTCAGGGTCATACAGGGCCTGAAGGAGCCATGGGGCCAACCGGA 270
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/organism="Tetraodon nigroviridis"
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/clone="0.48C07"
/clone_lib="A.
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AL311965.1 GI:9544833
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68.9%;
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3 (bases 1 to 651)
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Matches 51; Conservative
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Direct Submission
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FEATURES

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/organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6548"
/clone_lib="Taxon:6548"
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/ore="vector: Lambda Uni-Zab RR (Stratagene); Site_1:
/ore="vector Lambda Uni-Zab RR (Stratagene); Site_1:
/ore="vector lambda Uni-Zab RR (Stratagene); Site_1:
/ore="vector from the Row Infected dogs: CDNA was constructed and, using addaptors, was cloned unidirectionally into the vector from the EcoRI site to the XhoI site. The library has an unamplified titer of 1 x 1055 pfu/ml and an amplified, undiluted titer of 9 x 10EII pfu/ml. The average insert size of the unamplified library is 675 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCarter, J. Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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NTHe library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 388.
1. ods.tion/Qualiflers
1. ods.tion/Qualiflers
1. .1101
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/db_xxef="taxon:99883"
/clone="043116"
/clone_lib="A"
/note="Genoscope sequence ID : COAAO43BEO8C1-end : T7"
a 292 c 258 g 234 t 37 others
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Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                           Length 1101;
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Panagrolaimoidea, Strongyloididae, Strongyloides.
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Pred. No. 4.7;
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BE581564.1 GI:9832506
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68.9%;
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Brugia malayi.
Brugia malayi
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Matches 59; Conserv
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AW179840
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                                                    389
                   105
                                                                                                     RESULT 14
AW179710
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/lab_host="XLI-Blue MRF""
/note="Yector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I: Lymphatic filarial nematode parasite of humans.
mRNA was prepared from young adult worms isolated from
the peritoneal cavity of jirds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by Rhase H and DNA
pol I. The library has 6.2 x 105 independent recombinants
and the average insert size is approx.110lbp. The library
was constructed by Michelle Lizotte-Waniewski. The
library is available from Dr. S.A. Williams, email:
genome@neal.smith.edu."
                                                                                                                                                                                                                                                                                                                         AW675997 525 bp mRNA linear EST 27-APR-2000 SWYD25CAU13H04SK Brugia malayi young adult day 25 cDNA (SAW99MLW-BMYD25) Brugia malayi cDNA clone SWYD25CAU13H04 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes expressed in young adult day 25 of Brugia malayi
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 413585386
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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                                                                                                     0; Gaps
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                                                                    Length 454;
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5.2;
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                                                                Score 37;
Pred. No. 5
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(range, 100-1700).'
103 c 99 g
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AW675997.1 GI:7545483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onchocercidae; Brugia.
1 (bases 1 to 525)
                                                                Query Match 23.9%;
Best Local Similarity 62.4%;
Matches 58; Conservative
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1 Similarity 61.5%;
59; Conservative
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Brugia malayi
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                 136 a
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/dew_stage="young adult, twenty five days after infection"
/lab_host="xL1-Blue MRF"
/note="vector: Lambda Uni 2AP XR; Site_1: Eco RI: Site_2:
Xho I: Lymphatic filarial nematode parasite of humans.
Xho I: Lymphatic filarial nematode parasite of humans.
MRNA was prepared from young adult worms isolated from
the peritoneal cavity of jirds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by Rhase H and DNA
pol I: The library has 6.2 x 105 independent recombinants
and the average insert size is approx.110lbp. The library
was constructed by Michelle Lizotte-Waniewski. The
library is available from Dr. S.A. Williams, email:
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AW179710 575 bp mRNA linear EST 16-NOV-1995
SWYD25CAU02H05SK Brugia malayi young adult day 25 CDNA
(SAW99MLW-BMYD25) Brugia malayi CDNA clone SWYD25CAU02H05 5', mRNA
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Onchocercidae; Brugia.
1 (bases 1 to 575)
Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in young adult day 25 of Brugia malayi
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 4135833826
Email: genome@smith.edu
Seq primer: pBluescript SK.
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/clone="15"=Brugia malayi young adult day 25 cDNA
/saw99mLw-BmYD25)"
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1 Similarity 61.5%; Pred. No. 5.9;
59; Conservative 0; Mismatches
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                                                                                                                       AW179710
AW179710.1 GI:6445747
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ALILIANDA WILLIAMS
ALL Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413583826
Fax: 4135838
Fax: 4135838
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                                                                                                                                                                                    Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Orohocercidae; Brugia.
1 (bases 1 to 585)
Williams, S. A.
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Best Local Similarity 61.5%; Pred. No. 5.9;
Matches 59; Conservative 0; Mismatches
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sequence.
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                                                                                                                                                    Brugia malayi.
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105 ACCAGGTTTACCACAATATACAGGAGAAATAAGTGA 140 δλ

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378 ACCCGGTTTTCCAGGAAGACCACCAAGAATATGTGA 413

Search completed: February 20, 2003, 06:14:25 Job time : 395.859 secs

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Sequence 49, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 66, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 71, Appl
                                                                        ; Search time 12.4727 Seconds (without alignments) 6329.459 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-997-610-3

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US-09-935-868-25

US-09-954-868-25

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US-09-923-779-53

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US-09-923-779-68

US-09-923-779-68
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Maximum Match 100%
Listing first 45 summaries
                                                 nucleic search, using sw model
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Maximum DB
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                                                                          Run on:
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Sequence 6, Appliance 10, Appliance 11, Appliance 14, Appliance 141, Appliance 14
                 Sequence 5, Appli
Sequence 28, Appl
Sequence 4, Appli
Sequence 6, Appli
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Patent No. US20020156244A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.

TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
FILE REFERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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123 10 US-09-923-779-5

86 10 US-09-923-779-28

86 10 US-09-919-479-4

86 10 US-09-919-476-765

90 US-09-738-626-1

100 9 US-09-738-626-1

100 US-09-925-299-44

8 10 US-09-925-299-44

8 10 US-09-925-299-44

8 10 US-09-925-299-44

9 US-09-764-868-400

12 US-10-44-090-524

13 US-09-729-658B-1

14 US-09-729-658B-1

15 US-09-729-658B-1

16 US-09-729-658B-1

17 US-09-729-729-678B-1

18 US-09-729-658B-1

19 US-09-729-658B-1

10 US-09-729-729-678B-1

10 US-09-729-729-678B-1

10 US-09-729-729-11563

10 US-09-739-729-11563

10 US-09-789-729-11563

10 US-09-789-729-11563

10 US-09-789-729-11563

10 US-09-818-1242-7615

9 US-10-063-547-123
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (2)...(1381)
US-09-997-610-1
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121 TATACAGGAGAAATAAGTGAAATGACAAAATGCCC 155 

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Patent No. US2002015624A1

GENERAL INFORMATION:

APPLICANT: FOX. Brian

APPLICANT: HOLloway, James L.

TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN

TITLE OF INVENTION: AACRP13

FILE REFERENCE: 00-96

CURRENT APPLICATION NUMBER: US/09/997,610

CURRENT FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/253,924

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                     GENERAL INFORMATION:
APPLICANT: FOX, Brian
APPLICANT: FOX, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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LOCATION: (1)...(1377)
OTHER INFORMATION: Each n is independently A, T,
NAME/KEY: misc_feature
LOCATION: (1)...(1377)
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                                             Sequence 5, Application US/09997610
Patent No. US20020156244A1
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; OTHER INFORMATION: n = A,T,C or US-09-997-610-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)...(1731)
US-09-997-610-5
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RESULT 2
US-09-997-610-5
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TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using FILE REFERENCE: REG 203D CURRENT APPLICATION NUMBER: US/09/935,868 CURRENT FILING DATE: 2002-04-11 PRIOR APPLICATION NUMBER: PCT/US99/22045
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  Length 1377;
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APPLICANT: Fox, Brian
APPLICANT: HOlloway, James L.

TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP13
    DB 9;
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71.7%; Score 111.2; DB 9 64.5%; Pred. No. 7.3e-27; iive 22; Mismatches 33
                                                                                                                                                                                                                                                          121 TATACAGGAGAAATAAGTGAAATGACAAAATGCCC 155
                                                                                                                                                                                                                                                                                121 TATACAGGAGAAATAAGTGAAATGACAAAATGCCC 155
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CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PASTSEQ for Windows Version 3.0
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Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LCATION: (1)...(1731)
COTHER INFORMATION: n = A,T,C or G
US-09-997-610-7
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ORGANISM: Artificial Sequence
                                          Conservative
                      Best Local Similarity
Matches 100; Conserv
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US-09-935-868-25
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    Query Match
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TYPE: DNA
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Patent No. US20020164690al
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REC 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEC ID NO 23
SEC ID NO 23
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Pred. No. 0.054;
0; Mismatches 62; Indels 0
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Pred. No. 0.055;
0; Mismatches 62; Indels
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; Patent No. US20020165180A1
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 3477
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54.1%;
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Best Local Similarity 54.1%;
Matches 73; Conservative
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Matches 73; Conservative
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                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-09-935-868-23
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                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)
US-09-935-868-25
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 AGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACAGGTTTACCACAATATACAGGAGAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 CGCCCCCGAGCAGCAGCAGCAGTCTACCATGGCTCAAGAATCTCCCAAAAATTCAGCAGCA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 CCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCC 72
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Pred. No. 0.054;
0; Mismatches 63; Indels
                                                                                                                                          CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR PLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR PLICATION NUMBER: US/60/234,034
PRIOR PLICATION NUMBER: US/60/234,509
PRIOR PLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.7%;
Best Local Similarity 53.7%;
Matches 73; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 GAATTCCAGTGACTA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-954-531-1366
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Gaps

0;

Indels

31;

Length 415;

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46 GAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCA 105
                                                                                                                                                                                                                                                             156 GGACCTCCGGGGCCACCAGGACACCCAGGGCCTCCAGGTATAAGAGGGCCTCCAGGTATA 215
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Patent No. US20020076721A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Ralos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, MICHAEL D.
APPLICANT: RALOS OF SERVICE CANCER FILE REFERENCE: 210121.553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/09923779
Patent No. US20020076721A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
            ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB34-018-Q1-E1-B12
US-09-960-352-9137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.4%; Score 33.2; DB 10; 54.0%; Pred. No. 0.17;
                                                                                                                  Score 33.4; DB
Pred. No. 0.13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/923,779 CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 480, 498, 523, 539
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                           106 CCAGGTTTACCACATATACAGG 128
                                                                                                                                                                                                                                                                                                                                                    216 AGAGGAATACCAGGTTTGCCAGG 238
                                                                                                                    21.58;
62.78;
                                                                                                                    Query Match 21.55
Best Local Similarity 62.77
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Sequence 9137, Application US/09960352

Patent No. US2002013713941

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 9137

LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wesley C.
APPLICANT: Tao, Wengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt John C.
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1786
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                                                                                                                                                                                                                                       35;
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62.7%; Pred. No. 0.12;
iive 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 08-LIB34-023-Q1-E1-B7
                                                                                                                                                                                         DB 10;
0.096;
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                                                                                                                                                                                                                                                                                                                                                                               86 AAGTGGGCCTCCTGGTGCACCAGGTTTACC 116
                                                                                                                                                                                                                                                                                                                                                                                                                             854 CAAAAGGTCTCCCTGGGGCTCCAGGAATAGC 884
                                                                                                                                                                                         Score 35;
Pred. No.
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NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                    ch 22.6%;
1 Similarity 61.5%;
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
                                                                                                                  ; ORGANISM: Homo sapiens US-09-954-456-725
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 56; Conserv
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US-09-960-352-1786
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                                                                      3226
                                              SEQ ID NO 725
                                                                                          TYPE: DNA
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                                                                      LENGTH:
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Gaps

Length 549;

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US-09-923-779-53
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Sequence 51, Application US/09923779
Sequence 51, Application US/09923779
Septent No. US20020076721a1
SEBERAT INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER
TITLE OF INVENTION: UND DIAGNOSIS OF PANCREATIC CANCER
STLE REFERENCE: 210121.553
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 617
                                                                                                                                                                                                                                                                                 Length 561;
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Batent No. US20020076721A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Michael D.
TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
                                                                                                                                                                                                                                                                                                                            33; Indels
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                                                                                                                                                                                                                                                                            Query Match 21.4%; Score 33.2; DB 10; Best Local Similarity 61.6%; Pred. No. 0.17; Matches 53; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.2; DB 10;
Pred. No. 0.18;
0; Mismatches 33;
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 561
TYPE: DNA
OFGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 CTCCAGGACCTCCTGGTGCTATAGGT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 TACCACAATATACAGGAGAAATAAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 TACCACAATATACAGGAGAAATAAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 CICCAGGACCICCIGGIGCIATAGGI 489
                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 544, 550
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 581, 605
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-51
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Best Local Similarity 61.6%;
Matches 53; Conservative
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APPLICANT: PUTCH A.
APPLICANT: AU, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                             Length 648;
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0.18;
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Best Local Similarity 61.6%; Pred. No. 0.18;
Matches 53; Conservative 0; Mismatches 33;
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Pred. No. 0.18
0; Mismatches
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FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
ESCO ID NO 66
LENGTH: 648
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                                                                                                                                                                                                                                                           ; LOCATION: 642, 646
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-66
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; LCCATION: 517, 579, 581, 603, 649
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-53
                                                                                                                                                                                                                                                                                                                                                      Query Match 21.4%;
Best Local Similarity 61.6%;
Matches 53; Conservative (
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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5, Appli 5510466 3, Appli 3, Appli 1, Appli 1, Appli

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Sequence 1, Appli
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Sequence 635, App
Sequence 647, App
Sequence 624, App
Sequence 164, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 139, App
Sequence 5, Appli
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Sequence 3, A
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Patent No. 5866341

GENERAL INFORMATION:
APPLICANT: SPINELLA, Dominic
APPLICANT: BECHERER, Kathleen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
CORRESPONDENCE ADDRESS:
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Pred, No. 0.026;
0; Mismatches 62;
US-08-383-744-1
US-08-999-336-1
PCT-US96-01427-1
US-09-134-001C-635
US-09-134-001C-726
US-09-134-001C-726
US-09-173-581-16
US-09-173-581-16
US-09-173-581-16
US-09-173-591-16
US-09-173-591-16
US-09-173-591-16
US-09-174-095-5
US-08-776-971-139
US-08-776-971-139
US-08-776-971-139
US-08-744-795-5
US-08-744-795-5
US-08-744-795-5
US-08-744-795-1
US-08-666-3678-3
US-09-144-38-3
US-08-144-438-3
US-08-744-795-1
US-08-744-795-1
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,151A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Gen-Probe Incorporated 10210 Genetic Center Drive
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-410-8926
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SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
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Best Local Similarity 54.1
Matches 73; Conservative
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Sequence 3, Appli
Patent No. 5171840
Patent No. 5480796
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Sequence 2, Appli
Sequence 80, Appl
Sequence 141, App
Sequence 141, App
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Sequence 11, Appli
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Patent No. 5171840
Patent No. 5480796
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Sequence
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1: /cgn2_6/ptodate/2/lna/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*

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5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/lna/PcTUS_COMB.seq:*
                            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-029-34 B-20
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US-09-06-91-789A-141
US-09-59B-326-141
US-08-923-92A-7
US-09-342-6B1C-14
US-09-342-6B1C-14
US-09-342-6B1C-14
US-09-342-6B1C-14
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Listing first 45 summaries
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Maximum DB
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Gaps

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Sequence 3, Application US/08795473B Patent No. 6217858
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                                   888 GGAGTTCGGCCAAGG 902
   130 GAAATAAGTGAAATG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-795-473B-3
                                                                                     RESULT 4
US-08-795-473B-3
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TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
TITLE OF TIMENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL SITMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/907,650
FILING DATE: 02-JUL-1992
PRIOR APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35.8; DB 6; Length 14
Pred. No. 0.029;
0; Mismatches 62; Indels
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                                                                                                                                                                                                                                                   ; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
;STIMULATORY FEATOR-2
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Pred. No. 0.029
0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298,694
FILING DATE: 19-JAN-1989
SEQ ID NO:8:
LENGTH: 1404
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23.1%;
Best Local Similarity 54.1%;
Matches 73; Conservative
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Best Local Similarity 54.1%;
Matches 73; Conservative
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70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
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GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Mahot, Oritt
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
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Patent No. 6410009
GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
ATTLE OF INVENTION: A Pharmaceutical Composition for Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1486;
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0.029;
62;
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STREET: 1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.1%; Score 35.8; DF Best Local Similarity 54.1%; Pred. No. 0.029 Matches 73; Conservative 0; Mismatches
                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1037
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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1074 CTGTGTCATCCACGACGCCTGGAGCGGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 1133
                                            70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 2061;
                                                                                                                                                                                                                                                                     APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 0.033;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFFICATION:
ATTORNEY/AGENT INFORMATION:
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1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/907,650
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08795473B Patent No. 6217858
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APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
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New York
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Matches 73; Conserv
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;Patent No. 5480796
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STREET: 11
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Hepatitis B Virus (HBV) Infection 10
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TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
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0.033;
62;
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Pred. No. 0.029;
0; Mismatches 62;
 TITLE OF INVENTION: Hepatitis B Virus (HBV) Infe
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
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54.1%; Pred. No. 0.03:
:ive 0; Mismatches
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,856
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298,694
FILING DATE: 19-JAN-1989
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TELEPHONE: (212)-997-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.18;
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Best Local Similarity 54.1%;
Matches 73; Conservative
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Best Local Similarity 54.1'
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 GAAATAAGTGAAATG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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5171840-1
;Patent No. 5171840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2061
                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                       10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-439-856-3
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70 CCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 CCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGAGAAATA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                               10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCCAGG 75
                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence: SEQUENCE; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS US-09-029-348-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.4%; Score 33.2; DB 4; Length 1881; Best Local Similarity 54.0%; Pred. No. 0.22; Matches 68; Conservative 0; Mismatches 58; Indels 0
                                                                          Length 3319;
                                                                                                                   Indels
                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVORTION: 186 Human Secreted proteins;
FILE REPERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEO ID NOS: 20
SOFTWARE: PATENTIN VET. 2.0
                                                                                              0.04;
                                                                                                                   0; Mismatches
                                                                       23.1%; Score 35.8; 54.1%; Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09029348 Patent No. 6171827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                  Query Match
Best Local Similarity 54.1x
Local Similarity 54.1x
Conservative
                                                                                                                                                                                                                                                                                                                                                                                         1325 GGAGTTCGGGCAAGG 1339
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           unknown
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US-09-149-476-88/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-029-348-20
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LENGTH: 1881
                           US-09-439-856-2
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Patent No. 6410009
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blum, Herbert E.
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                      23.1%; Score 35.8; DB 4; Length 3319; 54.1%; Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                  62;
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1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
SEQUENCE CHARACTERISTICS:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1037
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
TYPE: nucled acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/09/439,856
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
US-08-795-473B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDARD STREET: 1140 ...
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 73; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-09-439-856-2
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60/043,313

1997-03-07 NUMBER: 60/038,621 1997-03-07 NUMBER: 60/040,626 1997-03-07 1997-03-07 NUMBER: 60/040,334 1997-03-07 NUMBER: 60/040,163 1997-03-07 NUMBER: 60/040,163 1997-03-07		55-23 66/047, 66/047, 55-23 66/047, 55-23 66/043, 4-11 66/043, 4-11 66/043, 4-11 66/043, 4-11 66/043, 4-11 66/043, 4-11 66/043, 4-11 66/043,
FILING DATE. APPLICATION DATE. PILING DATE. PILING DATE. PILING DATE. PILING DATE. PILING DATE. APPLICATION FILING DATE. APPLICATION FILING DATE. APPLICATION FILING DATE. APPLICATION FILING DATE.	FILING DATE PAPLICATION PAPLICATION FILING DATE APPLICATION FILING DATE	PILING DATE: APPLICATION APPLICATION FILING DATE: APPLICATION FILING DA
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EARLIER PILLNG DATE: 1997-04.11
EARLIER PILLNG DATE: 1997-06.22
EARLIER PILLNG DATE: 1997-06.23
EARLIER PILLNG DATE: 1997-06.2

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Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9388;
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMEBER: US/09/062,451
FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 31.4; DB 4;
51.8%; Pred. No. 1.5;
iive 0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: POTTER, Jane E. R.

REGISTATION UNBER: 210121.419C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9388 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8110 AGTTAAAAGGATAAATG 8094
                               Washington
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Matches 71; Conservative
                                                                                 ZIP: 98104-7092
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CITY: Seattle
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STATE: Washing
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STREET: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.3%; Score 31.4; DB 4; Length 1395; 51.8%; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                       EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-05
EARLIER APPLICATION NUMBER: 60/051,669
                     APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-991-789A-141/c
; Sequence 141, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, John M.
Reed, Steven G.
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Matches 71; Conserv
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                                                                                 Gaps
                                                                                                                         16 GTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCCAGG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group I TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
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                                       Length 9388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESENOID, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
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                                            DB 4;
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                                       Score 31.4; DI
Pred. No. 1.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08923992A Patent No. 6280738
                                     20.3%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.9%;
Best Local Similarity 57.1%;
Matches 56; Conservative (
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    136 AGTGAAATGACAAAATG 152
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                             Query Match
Best Local Similarity 51.8%
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US-08-923-992A-7
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Seed Intellectual Property Law Group PLLC STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                     Length 9388;
                                                                                                                                                                                                                                                                                                                                             66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: POLTEY. Jane B.R.
REGISTRATION NUMBER: 33,332
REFRENCE/DOCKET NUMBER: 210121.419D1
TELECOMMUNICATION INFORMATION:
TELEFRAM: (206) 622.4900
TELEFRAM: (206) 682-6031
INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                     Score 31.4; DE
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 141:
                                                        REFERENCE/DOCKET NUMBER: 210121.419C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 141, Application US/09598326
Patent No. 6423496
GENERAL IRFORMATION:
APPLICANT: Frudakis, Tony N.
                                                                                              TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 9388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9388 base pairs
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, John M.
Reed, Steven G.
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STRANDEDNESS: single
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51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8110 AGTTAAAAGGATAAATG 8094
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STATE: Washington
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Best Local Similarity
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US-09-598-326-141/c
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US-09-062-451-141
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Search completed: February 19, 2003, 22:59:00 Job time : 21.2324 secs

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Sequence encoding IL-6 receptor codi

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Human; gene; ss; gene therapy; genset metabolic gene; GMG-7A; GMG-7B; GMG-8; GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; heart disease; cardiac insufficiency; coronary insufficiency; high blood pressure; insulin sensitiser; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genset metabolic gene (GMG-9) cDNA sequence.
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/note= "No stop codon is given"
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ABK84606
ABL65415
AAS89670
AAH98343
AAH98411
AAD06578
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ABK44109
ABK44107
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ABK44126
ABK44113
ABK44128
ABK44129
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AAA26383
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AAD06575
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/*tag= a
/partial
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   15-JAN-2002; 2002WO-IB01215
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11. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

12. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

13. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

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19. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

20. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

21. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA1997.DAT:**

22. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA2001.DAT:**

23. /SIDS2/gcgdata/geneseq/geneseqn -embl_/NA2001.DAT:**

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1 atagtggtcatacctgtctt.....agtgaaatgacaaaatgccc 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA70701
AAZ40288
AAV04440
AAZ09202
AAV60296
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL44066
AAC01552
ABI99819
                                                                                                                                                                  US-09-997-610-1_COPY_2_156
                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
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328
6512
975
1035
1260
1486
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                                                                                                                                                                                                                                IDENTITY_NUC
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Match 1
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24.5
23.7
23.1
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23.1
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                                                                                                                                                                                    Perfect score:
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                                                                                                                                                                                                                                 Scoring table:
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Clone VGT22 of a g CDNA #49 encoding CDNA #47 encoding CDNA #51 encoding CDNA #56 encoding CDNA #58 encoding CDNA #69 encoding

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Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2001
                                                                                                                                                                                                   rectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse;
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ABI99819
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                                                                                                                                                              The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-9, GMG-9, GMG-10 and GMG-11). The GMC DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity; impaired glucose tolerance; insulin resistance: Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; and heart diseases (e.g. cardiac insufficiency, coronary insufficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present cDNA sequence encodes the human GMG-9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                   , 89 TGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
                                                                                                     obesity, impaired glucose tolerance, insulin resistance, Syndrome X, Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                    Treating or preventing a metabolic-related disease or disorder,
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                               Score 59; DB 24; Length 1338; Pred. No. 6e-09;
                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                           Sequence 1338 BP; 359 A; 288 C; 350 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 1550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giordano J;
                                                   Tanaka H;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                              Disclosure; Page 122–124; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                                                   Bihain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC01552 standard; cDNA; 328 BP.
                                                                                                                                                                                                                                                                                                                38.1%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-0200610
         16-JAN-2001; 2001US-262235P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                  Bour BA,
                                                                     WPI; 2002-557821/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45.
P-PSDB; AAG01546.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 149 AATGCCC 155
                                                                                 P-PSDB; AA015423
                                                                                                                                                                                                                                                                                                                                                                                                                    110 AATGCCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST;
                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEST ) GENSET
                                                  Erickson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC01552;
                                                                                                                                                                                                                                                                                                                                     Matches
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AAC01552
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs and all length cDNAs and genomic DNAs. 5' ESTs are also used to obtain full length energy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AGGCCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 CCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACCCC 72
New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.5%; Score 38; DB 21; Length 328; Best Local Similarity 52.2%; Pred. No. 0.02; Matches 71; Conservative 5; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi Y, Nagata T, Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 328 BP; 76 A; 77 C; 81 G; 88 T; 6 other;
                                                                                                                                                                          Claim 1; SEQ ID 1550; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABI99819 standard; cDNA; 6512 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-2001; 2001WO-JP04192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 ATAAGTGAAATGACAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GAAATTCCAGTGACTA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-034733/04.
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Example 1; Page 6-8; 10pp; Japanese.
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P-PSDB; AAY55071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09960113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1999;
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01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-1999
                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                       AAZ40288;
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                                                                                                                                                                                                                                                                                                                        831
                                                                                                                                                                                                                                                                                                                                                                   AAZ40288
ID AAZ4
                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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                                                    conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB19202 to AB19912, encoding the protein sequences in ABB57020 to ABB5714) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; interleukin-6 receptor; fungus; Pichia pastoris; PCR primer; ss; expression vector; immunoglobulin-like region; cytokine receptor region
                                                                                                                                                                                                                                                                                                  53 CTGGACCTCCAGCACACCCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTT 112
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "human IL-6R amino acids 20-344"
/note= "no start or stop codon is given at the 5'
3' ends of the sequence"
/transl_except= (pos:169..171.aa:Gly)
/transl_except= (pos:841..843,aa:Gly)
                                             The present invention describes a method for examining ischaemic
                                                                                                                                                                                             which are used in the exemplification of the present invention
                                                                                                                                                                                                                                          DB 24; Length 6512;
                                                                                                                                                                                                                   Sequence 6512 BP; 1553 A; 1798 C; 1950 G; 1211 T; 0 other;
                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                                                                                              113 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
                                                                                                                                                                                                                                         23.7%; Score 36.8; DB 61.5%; Pred. No. 0.16; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeasts transformed with IL-6 receptor gene
                      Claim 2; Page 2340-2352; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin 6 receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                AAA70701 standard; cDNA; 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..975
/*tag=
                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB15389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2000157280-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2000
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                                                                                                                                                                                                                                                                29:
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA70701;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                       Best
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The invention relates to the production of human interleukin-6 receptor (LL-6R) protein in the fungus Pichla pastoris. The fungus was transformed with an expression vector (PPIC9-A20LL) containing a generocding an IL-6R protein having an immunoglobulin-like region and cryckine receptor region and spanning amino acids from Leu20-Ala323. The human IL-6R region was PCR amplified using the primers AAAA70703. This sequence represents the coding region for the IL-6R protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the SR345 protein. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SR345 protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ATACCTGTCTTAATAACGCCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
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                                                                                                                                                                                                                                                                                                                                                                         Score 35.8; DB 21; Length 975;
Pred. No. 0.16;
0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                Sequence 975 BP; 208 A; 289 C; 290 G; 188 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ40288 standard; DNA; 1035 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohtomo
                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.1%;
Best Local Similarity 54.1%;
Matches 73; Conservative (
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98JP-0279876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SR345 coding sequence
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by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TWMT) method wherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                  70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                           768 ATATICGGGCTGAACGGTCAAGACATTCACAACATGGATGGTCAAGACCTCCAGCATCA 827
                                                                                                                                                                                                                                                                                                                                                                                                   828 CTGTGTCATCCACGACGCCTGGAGCGGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 887
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the development of a novel method of screening compounds for ability to bind a specific molecule. The method comprises contacting one or more compounds with a chimeric protein containing at least two domains, the 1st comprising a portion of the specific molecule, and the 2nd an immunoglobulin chain portion having one or more epitopes and/or immunoglobulin regions recognising an epitope. A binding partner complex between the chimeric protein and compound(s) is formed, separated out and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening of compounds for ability to bind specific molecules - using a chimeric protein in which the specific molecule is fused to an immunoglobulin chain
                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                             Length 1035;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                           Sequence 1035 BP; 210 A; 311 C; 315 G; 199 T; 0 other;
                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              Score 35.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; screening;
                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Pages 39-40; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUG-) CHUGAI BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spinella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV04440 standard; DNA; 1074
                                                                                                                                                                                                                             ch 23.1%;
l Similarity 54.1%;
73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin 6 receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; hu
library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTTCGGGCAAGG 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-503233/46.
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin 6
combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Becherer KA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9737220-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV04440;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                              protein.
                                                                                                                                                                                                                                                               datches
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This invention describes a novel gene which encodes a fusion protein of interleukin-6 (IL-6) receptor and bound with a gene sequence encoding for IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding protein has applications for the growth of bone marrow stem
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
contacted with a (in)directly labelled secondary molecule which binds the 2nd domain, and the label detected. Using the chimeric proteins, compounds can be rapidly screened for binding to an antigen, antibody, enzyme, enzyme substrate, receptor or ligand, e.g. in blomedical research and drug development. The method is especially intended for screening combinatorial libraries, but is also useful in screening bacterial/phage lysates, assays requiring specific binding partner interaction and obtaining binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
stem cell; platelet; reduced antigenicity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New interleukin-6 receptor-interleukin-6 fused protein and gene
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                                                                                                                                                                                               Length 1074;
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/note= "No start codon given"
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                Sequence 1074 BP; 223 A; 321 C; 324 G; 206 T; 0 other;
                                                                                                                                                                                              Score 35.8; DB 18;
Pred. No. 0.16;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IL-6 receptor/IL-6 fusion protein DNA.
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1..1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA209202 standard; DNA; 1260 BP.
                                                                                                                                                                                               Query Match 23.1%;
Best Local Similarity 54.1%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        888 GGAGTTCGGGCAAGG 902
                                                                                                                                                                                                                                                                                                                                                                                          130 GAAATAAGTGAAATG 144
                                                                                                                                   analogues of a compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY30938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
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Sequence 1486 BP; 305 A; 453 C; 439 G; 289 T; 0 other;
    and Ser177 to Arg, and mixtures of any of these.
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cells and platelets. Transmission of a signal of IL-6 to target cells for stimulation with reduced antigenicity is possible. This sequence encodes the IL-6 receptor/IL-6 fusion protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is a previously reported nucleotide sequence for human interleukin-6 (hIL-6). The invention relates to the finding that hIL-6 is essential for hepatitis B virus (HBV) infection. The invention provides a pharmaceutical composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the pS1 region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds to at least one of these sites and thereby prevents hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The coluble active agent is selected from glycoprotein 80 (gp80) having receptor sites which interact with hIL-6, soluble glycoprotein 130 receptor sites which interact with hIL-6, and having receptor sites which interact with hIL-6, hIL-6 derived peptide Gly17-Glu95, hIL-6 derived peptide Glu15-HiS165, a combined I and 2 hIL-6 mutant (mhIL-6 1+2), and mhIL-6 1+2 substituted with Phel71 to Leu
                                                                                                                                            70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                Gaps
                                                                                                                              ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated \,
                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-6; human; hepatitis B virus; HBV; infection; therapy;
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                                                                            Length 1260;
                                                                                                      Indels
                                                 Sequence 1260 BP; 341 A; 348 C; 321 G; 250 T; 0 other;
                                                                          Query Match 23.1%; Score 35.8; DB 20; Best Local Similarity 54.1%; Pred. No. 0.17; Matches 73; Conservative 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DAVI/) DAVIDSON C M.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin-6 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7; 51pp; English.
                                                                                                                                                                                                                                                                                                                        AAV60296 standard; DNA; 1486 BP
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                                                                                                                                                                                                                                                 130 GAAATAAGTGAAATG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; human; interleukin 6 receptor; Pichia pastoris; yeast; drug; myeloid stem cell; platelet; blood; ss.
                                                                                                                                                                                                       CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                   Gaps
                                                                                                      10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                     Yeast of Pichia Pastoris genus transformed by expression vector containing gene encoding fused protein of interleukin-6 receptor (II-6R) protein for amplifying myeloid stem cells and increasing platelets -
                                                      ö
     Length 1486;
                                            indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "IL-6R/IL-6 fusion protein"
/transl_except= (pos:169..171,aa:Glu)
/transl_except= (pos:841..843,aa:Gly)
     DB 19;
Score 35.8; DB; Pred. No. 0.18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-6R/IL-6 fusion protein coding sequence.
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1..1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA70763 standard; DNA; 1545 BP.
     23.1%;
54.1%;
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                          Best Local Similarity 54.1
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                          130 GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                         GGAGTTCGGGCAAGG 953
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Synthetic.
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       Query Match
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Sequence 2061 BP; 418 A; 631 C; 621 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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22-JAN-1988;
25-JAN-1988;
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 antagonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the fusion polypeptide H-IL-6 which contains an interleukin-6 acid linker which joins the carboxy terminus of human interleukin-6 receptor (IL-6R) with the amino terminus of human interleukin-6 (IL-6). Such conjugates could be used to modulate interactions between proteins, particularly to overcome interrupted interactions caused by an incomplete interleukin-6 (IL-6) receptor. These constructs derived from IL-6 and its receptor, can also be used for an vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
                                                                                                                                                                                                                                                                            Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
                                                                                                                                                                                                                                                        Human fusion polypeptide H-IL-6 DNA containing a 18 amino acid linker.
                                                          70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                            Gaps
                                              10 ATACCTGTCTTAATAACGCCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
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for
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0
         Length 1545;
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                            Indels
        21;
                                                                                                                                                                                                                                                                                    protein interaction; therapeutic; antagonist; ss.
                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ANGE-) ANGEWANDIE GENTECHNOLOGIE SYSTEME GMBH.
       Score 35.8; DB Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                        /product= H-IL-6
/note= "fusion polypeptide"
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vivo expansion of human stem cells
                                                                                                                                                                                              AAT97848 standard; DNA; 1627 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 1; 19pp; German.
       ch 23.1%;
1 Similarity 54.1%;
73; Conservative
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                                                                                                                                             831 GGAGTTCGGGCAAGG 845
                                                                                                                                                                                                                                                                                                                                              34..1611
/*tag= 5
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                                                                                                                         130 GAAATAAGTGAAATG 144
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                                                                                                                                                                                                                                                                                                                                                                 34..90
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                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW36846.
                                                                                                                                                                                                                                     25-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9732891-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-1996;
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rose-John S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                 AAT97848;
                                                                                                                                                                          RESULT 10
AAT97848
                           Matches
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70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                     Gaps
                                                                                                                               10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor protein for human B cell stimulating factor-2 - obtd. by recombinant DNA techniques and used as diagnostic, prophylactic or therapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding a receptor protein for human B cell stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The cDNA in AAN90340 was derived from monocyte cell line U937. Isolated BSF2 receptor and DNA encoding it are claimed, as are (b) expression vectors; (c) host organisms; (d) antibodies; and (e) hybridomas.
                                                                                    ;
                                          Length 1627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell; immune disorder; therapy; diagnosis; prophylaxis; ss
                                                                                    Indels
Sequence 1627 BP; 388 A; 450 C; 481 G; 308 T; 0 other;
                                                                                  62;
                                          DB 18;
                                        Score 35.8; DB
Pred. No. 0.19;
0; Mismatches
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/*tag= a
/note= "SQ claimed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN90340 standard; cDNA; 2061 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89JP-0017461.
88JP-0012387.
88JP-0012599.
88JP-0194885.
89JP-0009774.
                                          23.1%;
                 Query Match
Query Match
Best Local Similarity 54.1",
Best Anna 73; Conservative
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                                                                                                                                                                                                                                                                                                    130 GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                             (BSF2 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-214667/30.
P-PSDB; AAP90284.
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1053 CTGTGTCATCCACGACGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 1112
             CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor protein for human B cell stimulating factor-2 - used f developing prophylactic, therapeutic and diagnostic agents for associated disorders.
                                                                                                                                                                                                   DNA contg. region encoding BSF2 receptor.
                                                                                                                                                                                                                        cell stimulating factor-2 receptor;
                                                                                                                                                                                                                                                                Location/Qualifiers
247..1650
/*tag= a
250..312
/*tag= b
1330..1404
/*tag= c
                                                                                                                                  BP.
                                                                                                                                AAN90847 standard; DNA; 2087
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Best Local Similarity 54.1%;
Matches 73; Conservative
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88JP-0012599.
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89JP-0007461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KISH/) TADAMITSU KISHIMOTO
                                                                                                                                                                             (first entry)
                                                                            1113 GGAGTTCGGGCAAGG 1127
                                                       GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-264012/37.
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                                                                                                                                                                                                                                               Homo sapiens.
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04-AUG-1988;
14-JAN-1989;
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                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-1989;
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                                                                                                                                                                                                                                                                                               Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
transmembrane; multiple myeloma; binding; ability; signal transfer;
disease; intracellular; ss.
                                                       1074 CTGTGTCATCCACGACGCCTGGAGCGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 1133
                                                                                      CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the receptor lacking either the immunoglobulin-like domain or the transmembrance and intracellular domain have IL-6 binding ability and signal transfer ability. Either the full length or truncated IL-6 receptors may be used for diseases caused by IL-6 such as multiple
                         Gaps
                                           10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes an interleukin-6 (IL-6) receptor. Varients of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caused
 Length 2061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New interleukin-6 receptor deriv. - for treating diseases by IL-6, e.g. multiple myeloma
                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2066 BP; 420 A; 642 C; 615 G; 389 T; 0 other;
  DB 10;
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                      62;
23.1%; Score 35.8; DB llarity 54.1%; Pred. No. 0.21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.8; DB
Pred. No. 0.21;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
226..1632
/*tag= a
                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                           IL-6 receptor coding sequence
                                                                                                                                                                                                          AAQ41746 standard; DNA; 2066
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54.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-025521
                                                                                                                                              73; Conservative
                                                                                                                               130 GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-161739/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOYJ ) TOSOH CORP.
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Best Local Similarity
          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR37215.
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                                                                                                                                                                                                                                                     13-SEP-1993
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                                                                                                                                                                                                                                 AAQ41746;
  Query Match
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                      Matches
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monocyte U937 cell line.

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                                                 The DNA contains a region encoding the BSF2 receptor derived from a monocyte U937 cell line. It is used to produce large amts. of receptor, and may also be used as a probe for screening related genes. Regions b and or ep
                                                                                                                                                                                                                                                                                                                                                                           CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             10 ATACCTGTCTTAATAACGCCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                 Sequence 2087 BP; 426 A; 646 C; 621 G; 394 T; 0 other;
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                                                                                                                                                                                                                                                                                         0; Mismatches
Disclosure; fig 3.1-3.5; 76pp; English.
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1325 GGAGTTCGGCCAAGG 1339
                                                                                                                                                                      Homo sapiens.
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                                                                                               02-FEB-1999
                                                                                                                                                 therapy; ss.
                                                                                                                                                                                                               20-AUG-1998
                                                                         AAV60295;
                                RESULT 15
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1074 CIGIGICATCCACGACGCCTGGAGCGGCCTGAGGCACGTGCTGCTGCTGCTGCCCAGGA 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1265 CTGTGTCACGACGCCTGGAGCGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-6; IL; receptor; antisense oligonucleotide; inhibition; gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis; rheumatoid arthritis; endotoxic shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 CCCAGGCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-sense oligo:nucleotide inhibitor against human IL-6R expression - for treatment of e.g. tumours, cancers, rheumatoid arthritis, psoriasis, endo:toxic shock, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ATACCTGTCTTAATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense oligonucleotides may be used to inhibit the expression of the interleukin-6 receptor. Inhibition of expression of the IL-6 receptor is useful in the treatment of kidney tumours, myeloma, Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic shock. The antisense oligonucleotides are administered at a dosage of 0.1-100mg/kg, pref. 0.1-50 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3319 BP; 735 A; 937 C; 960 G; 687 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                          /product= Interleukin-6 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.8; DB Pred. No. 0.25; 0; Mismatches
                                                                                                                                                          Interleukin-6 receptor coding sequence.
                                                                                                                                                                                                                                          Location/Qualifiers
438..1844
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 17-21; 32pp; Japanese.
                                                                                            AAT31441 standard; cDNA; 3319 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.1%;
Best Local Similarity 54.1%;
Matches 73; Conservative (
                                                                                                                                                                                                                                                                                                                                        95WO-JP02587
                                                                                                                                                                                                                                                                                                                                                            95JP-0210739
                                                                                                                                                                                                                                                                                                                                                                       94JP-0313167
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                               Koishibara Y, Kuromaru K;
                                        1134 GGAGTTCGGGCAAGG 1148
                    130 GAAATAAGTGAAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATAAGTGAAATG 144
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                                                                                                                                     28-NOV-1996
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                              WO9618416-A1
                                                                                                                                                                                                                                                                                                                                       15-DEC-1995;
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                                                                        RESULT 14
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This is a previously reported nucleotide sequence for human interleukin-6 (hIL-6) receptor mRNA. The invention relates to the finding that hIL-6 is essential for hegatitis B virus (HBV) infection. The invention provides a pharmaceutical composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the pS1 region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds of the set one of these sites and thereby prevents hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The soluble active agent is selected from glycoprotein 80 (gp80) having receptor sites which interact with hIL-6, soluble glycoprotein 130 receptor sites which interact with hIL-6, soluble glycoprotein 130 derived peptide Gln15-HiL-6 derived peptide Gln15-HiL-6 derived peptide Gln15-HiS-6, a combined I and 2 hIL-6 mutant (mhIL-6, H-2), and mhIL-6, H-2 substituted with Phel71 to Leu mutant (mhIL-6, H-2), and mhIL-6, H-2 substituted with Phel71 to Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated by human interleukin \boldsymbol{6}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                               Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
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Pred. No. 0.25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DAVI/) DAVIDSON C M.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6a-b; 51pp; English.
                                                                                                                                                                                                                          Human interleukin-6 receptor cDNA.
AAV60295 standard; DNA; 3319 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
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                                                                                                                                                     (first entry)
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Best Local Similarity 54.1
Matches 73; Conservative
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Search completed: February 19, 2003, 22:56:26 Job time : 61.6445 secs

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February 19, 2003, 23:16:26 ; Search time 494.184 Seconds
(without alignments)
9128.055 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htgo_other:*
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Maximum DB :
                                                       OM nucleic
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                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a

ньзигру 145880 bp DNA linear PRI 12-DEC-1999 Human DNA sequence from clone RPI-302b9 on chromosome 22 Contains GSSs, complete sequence.

282198 282198.2 GI:6572207

ACCESSION VERSION KEYWORDS SOURCE

LOCUS .

RESULT 1 HS302D9 Homo sapiens. Homo sapiens

ORGANISM

ALIGNMENTS

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145880) Bridgeman, A.

Direct Submission

REFERENCE AUTHORS TITLE

J04694 Mus musculu AF159387 Mus muscu X61045 Hydra N-COL AC096135 Rattus no Z78064 Caenorhabdi U5221 Human arfap 230348 B.mori mRNA X65120 H.sapiens C AJ005395 Rattus no X70369 R.norvegicu X72580 Homo sapien X99519 Herpesvirus AE010554 Fusobacte AC120069 Rattus no AX331924 Sequence AR145506 Sequence X58298 Human mRNA E35612 IL-6 recept A93714 Sequence 2 A93714 Sequence 1 E04823 CDNA encodi E02673 CDNA encodi AR145505 Sequence AX399205 Sequence Z22964 C.elegans a U53342 Caenorhabdi AC110674 Tetraodon 297635 Human DNA s AJ318214 Danio rer AJ420010 Ostertagi U22327 Caenorhabdi X06777 Mouse mRNA AX306181 Sequence Z78064 Caenorhabdi AL132952 Caenorhab Yeast trans AR031384 Sequence BD009752 Compositi E28089 Novel IL-6 AX333243 Sequence X60382 H.sapiens C G28608 human STS X12830 Human mRNA score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description 10 MMCOLA4 6 AX306181 10 MUSCOL1A4A 10 AF169387 SUMMARIES HS10A1COL RNJ005395 HVSX99519 CEU22327 CECOLA2IV U53342 DRE318214 OOS420010 HSU52521 BMCOLGMR AR031384 BD009752 AE010554 AC120069 CEY51H4A RNPRO1C AC110674 AX331924 HSCOLX3 HSNCOL1 CEF57B1 HSIL6R 900 DB 71.6 145880 26.2 5851 25.3 87100 1486 1486 11942 34671 123789 36532 269619 1993 Match Length 1260 95492 23.1 23.0 23.0 22.8 22.7 22.7 Score 37. 8 ပ υυ 0 0 0

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/note="MLT1B repeat: matches 119. .178 of consensus" 15728. .16027
                                                                                                                                               /note="AluJb repeat: matches 9. .290 of consensus" 775. .8060 //note="AluJb repeat: matches 1. .295 of consensus" 8414. .851 //note="L2 repeat: matches 2553. .2706 of consensus" 8914. .9030 //note="MIR repeat: matches 147. .262 of consensus" 9110. .9280 //note="MIR repeat: matches 91. .262 of consensus" 9110. .9280 //note="MIR repeat: matches 91. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Alusg1 repeat: matches 2. .114 of consensus"
15669. .15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2275 of consensus'
                                                                  .302 of consensus"
                                                                                                           .77 of consensus"
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                      .23 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    words "MIR repeat: matches 49. .233 of consensus"
5071. .15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .99 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .425 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                     matches 3. .161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .302 of
                                                                                                                                                                                                                                                                                                                                                                          .144 of
                                                                                                           23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 79. ...
10718. .11310
/note="match: GSS: Em:B14024"
10784. .1120
/note="match: GSS: Em:B43656"
11838. .11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 173.
14597. 15201
/note="match: GSS: Em:AQ553482"
14616. 15060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 174. 3398. 13698 note="Alusp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15071. .15188
/note="12 repeat: matches 2112.
15104. .15399
                         note="MADE1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 141.
14589. .14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1B repeat: matches 1.
15490. .15662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ701486"
complement(10249, .10706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 1988.
12444. .12642
                                                                                                                                                                                                                                                                                                                                                                                                                                       9820. .10225
/note="MSTB repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.
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                                                                                                                                                                                                                                                                                                                                                                          matches 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Em: AQ225495'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 20.
12174. .12445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 63.
13017. .13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 76.
13806. .13919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 77.
13945. .14060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(10179. 10678)
/note="match: GSS: Em:B56592"
complement(10204. 10728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: G49301"
                                                                                                             matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matches
                                           686. .6987
note="AluSx repeat:
                                                                                      /note="MADE1 repeat: 7482, .7754
                                                                                                                                                                                                                                                                                                                                                                                          9521. .9679
/note="FAM repeat:
                                                                                                                                                                                                                                                                                                                                                 9283. .9412
/note="MIR_repeat:
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10312. .10383
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13331. .13397
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14061. .14367
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4868. .15040
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                  CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonery requests: clonerquest@sanger.ac.uk

On Dec 13, 1999 this sequence version replaced gi:3164067.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSROT; Tr., TREMBL; Wp., WORNEEP; Information on the WORNEEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22 Mapping Group. Further information can be found at the Roswell RTH-30209 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP1-302D9 The true left end of clone CTA-282F2 is at 69682 in this sequence. The true right end of clone CTA-41562 is at 55167 in this sequence.
  Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323. 3343
note="MLT1E repeat: matches 116. .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4279. .4485
//note="MLTIE repeat: matches 359. .568 of consensus"
5073. .5176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .209 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="MER5A repeat: matches 26. .187 of consensus"
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/note="L2 repeat: matches 2579. .2705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2350. .2660
/note="Aluso repeat: matches 3. .309 of consensus"
2684. .2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .312 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684. .2981
note="AluSq repeat: matches 2. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572. .759
/note="MER3 repeat: matches 1. .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 24. .160 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .073. 5176
'note="52 copies 2 mer ct 78 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188. .245
/note="MER3 repeat: matches 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46. 571
'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          033. .1336
note≂"AluSp repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-1"
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'note="MIR r
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'note="L2 re
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us-09-997-610-1\_copy\_2\_156.rge

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Query Match
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/note="match: GSS: Em:AQ005063"
/note="match: GSS: Em:B14179"
19537- .20290
/note="HEKYPH21 repeat: matches 4657. .5784 of consensus"
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/note="77 copies 2 mer tt 70 conserved"
/note="AluSg1 repeat: matches 1. .306 of consensus"
21239. .21553
/note="HUBERS-P3 repeat: matches 4410. .4713 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fowler, S.J., Jose, S., Zhang, X., Deutzmann, R., Sarras, M.P. Jr. and Boot-Handford, R.P.
Boot-Handford, S.P.
Boot-Handford, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydra vulgaris
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
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                                                             /note="MLT1B repeat: matches 178. .390 of consensus"
16546. .16854
                                                                                                                                                                                                                               /note="MER66-internal repeat: matches 4548. .4919 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12538. .22850
"note="AluSp repeat: matches 1. .313 of consensus"
12851. .23801
/note="Alusc repeat: matches 1. .299 of consensus"
16028. .16245
                                                                                                                                                                                                                                                                                                                                                         /note="AluJb repeat: matches 1. .311 of consensus"
18713. .19133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .364 of consensus"
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/note="MER66-internal repeat: matches 3017. .3102
                                                                                                     /note="Alux repeat: matches 1. .300 of consensus"
18296. .18323
                                                                                                                                                           8296. .18323
note="MSTA repeat: matches 2. .29 of consensus"
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        CCAGCACCCCCAGGCCCCCCAGAAGTGGGCCTCCTGGTGCACCAGGT
        111

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        34846
        CCAGCACACCCCAGGCCCCCCAGAAGAAGTGGGGCCTCCTGGTGCACCAGGT
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/note="THEIB repeat: matches 1. .364 of cons
22302. .2537
/note="MER66-internal repeat: matches 2186.
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/note="MER66-internal repeat: matches 1210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20317, .20382
/note="33 copies 2 mer ta 68 conserved"
20513, .20666
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23905. .23
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VERSION
KEYWORDS
SOURCE
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IGPOGPOGDKGDOGOVIGPKGETGAIGKKGETGQDGLKGRDGIGKQGANGEKGEKGN
SVVGLPGDPGEKGSPGEKGKDGISGKQGKPGPPGKDGVDGTPGKDGLPGNPGPEGPKG
EKGVTGPTGLDGEKGEPGYSGQKGAKGETGVRGKPGATSNVMGPKGNRGESGAKGEPG
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RGDVGERQFASIGNTGISONOSPRESGSPPQIKGEPGSVGSIGFRGSKGERGKGER
GSTLKGNPGPEGPREPPGPAGKNY ILDLEVGPLGERPTKGEPGEDGPKGDRGDIG
ETGSQGTKGEKGVPGSKGEKGEQGLEGPKGLEGRVGLAGSKGDKGIKGVIGKPPGD
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VLAVHSQSELDPKCPDGWENLWTGFSFLMYNSAGAQGSGQLLSSSGSCLEDFRVNPYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNHTTKWTIWIVLIFTLHSCLVFTQLCGGGGCNQCSNVCVGQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSHGRPGDEGRQGEPGLPGCNGTKGD1GPPGPRGKDGVQGPSGLPGP1GPPGEPGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEAGQDGQKGEKGDKGE1GSAGPSG1QGEKGD1GATGAAGTKGEPGSDGSLGSPGQKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATKLKGQKGEPGPKSQDGPAGDPGTKGDKGESGKAGRMGPQGLRGEKGARGDSNITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRGSVGLPGFKGP1GEPGFPGGEGPAGRPGEKGDGGAPGLQGEVGARGKVGPPG1PG1
                                                                                                                          of Manchester, Oxford Road, Manchester M13 9PT, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   /product-"type IV collagen alpha 1 chain precursor"
/protein_id="AAG40729.1"
/db_xref="G1:11875612"
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4642. .5325
/note="Region: non-collagenous domain"
942 c 1638 g 1318 t
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  Chem. 275 (50), 39589-39599 (2000)
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Pred. No. 0.12;
0; Mismatches
                                                                                                                                                                                                                           1. .5851
/organism="Hydra vulgaris"
/db_xref="taxon:6087"
                                                                         2 (bases 1 to 5851)
Fowler, S.J. and Boot-Handford, R.P.
Direct Submission
Submitted (27-JUN-2000) School of
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/note="Region:
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7747. .7889
/note="LIPA8 repeat: matches 6022. .6163 of consensus"
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21870. .22105
/note="Alusx repeat: matches 1. .286 of consensus"
22218. .23368
/note="HAL1 repeat: matches 1427. .1589 of consensus"
                                                                   84. .304 of consensus"
                                                              3517. 3704.
/note="LTR41 repeat: matches 597. .772 of consensus"
4053. .4193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7890. .7953
/note="MER33 repeat: matches 258. .322 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 46. .190 of consensus"
17702. 18055
/note="L2 repeat: matches 2385. .2749 of consensus"
18228. .18337
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT11 repeat: matches 57. .410 of consensus"
1505. 16078
/note="MRSA repeat: matches 1. .183 of consensus"
16546. 16698
                                                                                                                                     4053. 4193

Anote—"LTR41 repeat: matches 1. .135 of consensus"

4911. .5196

Anote—"AluSg repeat: matches 1. .284 of consensus"

Complement(<5103. .>5396)

Anote—"match: STS G07800"

<5193. .>5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2705 of consensus"
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3286. .3506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9783. .9866
//note="MIR repeat: matches 60. .148 of consensus"
10330. .10532
//note="MIR repeat: matches 13. .224 of consensus"
11250. .11290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //note="MIR repeat: matches 18. .183 of consensus"
12352. .12693
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20428. .20785
/note="LiMB3 repeat: matches 5813. .6185 of const
20855. .20914
                                                                                                                                                                                                                                                                                    J197. .5248
/note="13 copies 4 mer taga 98% conserved"
5197. .5246
/note="25 copies 7
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/note="12 copies 4 mer acac 98% conserved"
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11947. 12101
                         3286. .3506 . ---- matches /8.
/note="AluSg/x repeat: matches 3517. .3704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800. .6807
note="Single clone region"
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24727. .24778
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/note="2 copies 168
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/note="27 cc
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On May 14, 1999 this sequence version replaced gi:4678473.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBLS. Sw.: SWISSRROT; Tr:, TREMBL.
IMPORTANT: This sequence is not the entire insert of clone 438L4.
It may be shorter because we arrange for a small overlap between neighbouring submissions.

The true left end of clone 505B13 is at 87001 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the father the father is made to resolve all sequence the father. Annotation using the 'unsure' father.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 438L4 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pcyPAC2.
                                                              HS438L4 B7100 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 438L4 on chromosome 1p36.2-36.3 Contains ESTs, STS and GSSs, complete sequence.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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note="LiM4c repeat: matches 1716. .1890 of consensus"
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Znote="LiM4c repeat: matches 1557. .1716 of consensus"
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/note="L2 repeat: matches 2427. .2508 of consensus"
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// Anote="Alusx repeat: matches 2. .300 of consensus"
2527. .2709
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/note="7 copies 4 mer caca 93% conserved"
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'note="13 copies 2 mer ca 96% conserved"
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/db_xref="taxon:9606"
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/clone="RP3-438L4"
/clone_llb="RPCI-3"
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                                                                                                                                                              297635.10 GI:4835272
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/note="26 copies 2 mer gt 90% conserved"
30752. .30915
/note="MER20 repeat: matches 31. .197 of consensus"
                                                                                                                                                    .2705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1517 of consensus"
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                                                                                                                                                                                                                  .143 of consensus"
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29198. .29294

70048- .29294

70048- .29304

70048- .2930
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/note="68 copies 2 mer ac ...
/note="17.26438
/note="23 copies 4 mer caca 72% conserved"
n 26348. 26439
/note="46 copies 2 mer ac 73% conserved"
26551. 26666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="120 copies 2 mer ac 83% conserved" 26696. 26696 mer ac 77% conserved" 26699. 26734 //note="18 copies 2 mer ca 81% conserved" 27002. 27113 mer ac 60% conserved" 27117. 27146
                                                                             /note="match: GSS A0312336 clone R-103110" 25668. 25753 //note="L2" repeat: matches 2622. .2705 of co 26036. .26064 //note="MIR repeat: matches 115. .143 of col
                                                                                                                                                                                                                                                                                                                                                                                                                              26551. .26606
/note="28 copies 2 mer ac 73% conserved"
26608. .26647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //note="L2 repeat: matches 2607.
10005. .30056
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         .23 copies 2 mer ac 100% .25627
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17281 CAACAATTAATT 17270

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Ostertagia ostertagi partial mRNA linear INV 22-NOV-2001 Ostertagia ostertagi partial mRNA for collagen (col gene). AJ420010 AJ420010. GI:17065950 col gene; collagen. Ostertagia ostertagi.
                                                                                                                                                                                                                       Phylogenetic analysis on vertebrates fibrillar collagen enlights zebrafish a3(1) position and evidenced an evolutionary link between collagen alpha chains and Hox clusters
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                             DRE318214 1395 bp mRNA linear VRT 14-AUG-2001
Danio rerio partial mRNA for collagen type I alpha 3 chain (collA3
                                                                                                                                                                                                                                                                                                                                       Extracellular matrix and du Vercors Lyon, 69367,
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 1395)

Morvan-Dubois, G., Le Guellec, D., Garrone, R., Zylberberg, L. and
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zebrafish.
Danio rerio
                                                                                                                                                                                                                                                                                         Orbases 1 to 1395)
Morvan-Dubois,G.
Direct Submission
Submitted (11-JUN-2001) Morvan-Dubois G.,
development, IBCP UMR5086-CNRS, 7 passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="extracellular matrix"
/codon_start=3
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Pred. No. 0.59;
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/db_xref="taxon:7955"
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1. .1395
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                                                                       ĀJ318214
AJ318214.1 GI:15149947
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Best Local Similarity
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RESULT 4
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/chromosome="x"
join(603. .625,843. .897,1095. .1157,1532. .1631,1954. .2142,
2643. .2818,2870. .2947,3068. .3175,3206. .3316,3714. .3830,
                                                                                                                                                                                                                                                                                                                                                                        CEU22327 9448 bp DNA linear INV 26-MAR-1995 Caenorhabditis elegans alpha2(IV) collagen gene, complete cds.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
                                                De Maere, V., Vercauteren, I., Claerebout, E. and Vercruysse, J. Identification of potential protective antigens with local antibody
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Submitted (13-NOV-2001) De Maere V., Parasitology, University
Ghent, Salisburylaan 133, 9820 Merelbeke, BELGIUM
Location/Qualifiers
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Sibley,M.H., Johnson,J.J., Mello,C.C. and Kramer,J.M.
Genetic identification, sequence, and alternative splicing
Generorhabditis elegans alpha 2(IV) collagen gene
J. Cell Biol. 123 (1), 255-264 (1993)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 others
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    9448
    /organism="Caenorhabditis elegans"

                                                                                                                                                                                                                              /organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
1. .287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 3;
Pred. No. 0.59;
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University, Chicago, IL 60611, USA
Location/Qualifiers
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/db_xref="taxon:6239"
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1 Similarity 58.5%;
62; Conservative
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                                                                                                                 2 (bases 1 to 287)
De Maere, V.
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U22327.1 GI:732525
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                                                                                                 Unpublished
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CEU22327
LOCUS
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SOURCE
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                                                                                                                                                                                                     FEATURES
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3877. .4041,4091. .4362,4410. .5271,5324. .5996,6274. .7088,7134. .7365,7419. .8210,8293. .8756,8815. .8907)
/note="basement membrane collagen"
                                                                                                                                                                                                                                                                                                                                                                IGSIGPKGDPGDLGSVGPPGPPGPPEFFFGSGSIVGPRGNPGEKGDKGDIGAMGPAGPP
GPIASTMSKGTIIGPKGDLGEKGEPGEGGGRGYPGNGGLSGQPGLPGMKGEKGLS
GPAGPRGKEGRPGNAGPPGFKGDRGLDGLGGIPGLPGQKGBAGYPGRDGPKGNSGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSGLPGVPGFKGETGLPGYGQPGEKGLPGIPGKAGRQGAPGSPGQDGLPGFPGMK
GESGYPGQDGLPGRDGLPGVPGQKGDLGQSGQPGLSGAPGLDGQPGVPGIRGDKGQG
LPGIPGDRGMDGYPGQKGENGYPGQPGLPGGEKGFAGTPGFPGLKGSPGYPGQDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPGQPGSPGFPGLKGDAGLPGLPGTPGLEGQRGFPGAPGLKGGDGLPGLSGQPGYPG
EKGDAGLPGVPGREGSPGFPCQDGLPGVPGMKGEDGLPGLPGVTGLKGDLGAPGQSGA
PGLPGAPGYPGMKGNAGIPGVPGFKGDGGLPGLNGPKGEPGVPGMPGTPGMKGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAVCEAPANTIAVHSQTIQIPNCPAGMSSLMIGYSFAMHTGAGAEGGGGSPSSPGSCL
EDFRATPFIECNGARGSCHYFANKFSFWLTTIDNDSEFKVPESQTLKSGNLRTRVSRC
QVCVKSTDGRH"
                                                                                                                                                                                     /translation="MKQRAALGPVLRLAILALLAVSYVQSQATCRDCSNRGCFCVGEK
                                                                                                                                                                                                              GSMGAPGPQGPPGTQGIRGFPGPEGLAGPKGLKGAQGPPGPVGIKGDRGAVGVPGFPG
NDGGNGRPGEPGPPGAPGWDGCNGTDGAPGIPGRPGPPGMPGFPGPPGMPGLKGEPAI
                                                                                                                                                                                                                                                                 GYAGAPGEKGDGGMPGMPGLPGPSGRDGYPGEKGDRGDTGNAGPRGPPGEAGSPGNPG
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KDGFPGLPGQKGESGLSGLPGAPGLKGESGMPGFPGAKGDLGANGIPGKRGEDGLPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGRDGQPG1PGLKGEVGGAGLPGQPGFPG1PGLKGEGGLPGFPGAKGEAGFPGTPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCC
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collagen; collagen alpha 1 type IV.
caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota: Metazoa: Nematoda; Chromadorea: Rhabditida;
Rhabditidaea: Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 69 to 8997)
Sibley,M.H., Johnson,J.J., Mello,C.C. and Kramer,J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9448;
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Pred. No. 0.93;
0; Mismatches 57;
                                                                                                 /product="alpha2(IV) collagen"
/protein_id="AAA64312.1"
/db_xref="GI:732526"
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55.88;
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les 72; Conservative
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ACCESSION
VERSION
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AUTHORS
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SOURCE
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GYAGAPGEKCDGGMPGMPGLPGPSGRDGYPGEKGDRGDTGNAGPRGPPGEAGSPGNPG
IGSIGPKGDPGDIGAMGPAGPPGPIASTMSKGTIIGPKGDLGEKGEKGEPGEGGGRGY
PGNGGLSGQPGLPGMKGEKGLSGPAGPRGKEGRPGNAGPPGFKGDRGLDGLGGIPGLP
                                                                                                                                                                                                                                                       GOKGEAGYPGRDGPKGNSGPPGPPGGGTFNDGAPGPPGLPGRPGNPGPPGTDGYPGAP
GPAGPIGNTGGPGLPGYPGNEGLPGPKGDKGDGGIPGAPGVSGPSGIPGLPGPKGEPG
YRGTPGQSIPGLPGKPGLDGAPGRKGENGLPGVRGPPGDSLNGLPGAPGQRGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLMDGYSLLY I EGNEKSHNODLGHAGSCLQRESTMPFLFCDFNNVCNY ASRNEKSYWL
STSEA I PMMPVNEREI EPY I SRCAVCEAPANT I AVHSQT I QI PNCPAGWSSLWI GYSF
AMHTGAGA EGGGQSPSSPGSCLEDFRAT PFI ECNGARGSCHY FANK FSFWLTT I DNDS
                                                                                                                       /translation="mKQRAALGPVLRLAILALLAVSYVQSQATCRDCSNRGCFCVGEK
GSMGAPGPOGPPGTOGIRGFPGPEGLAGPRGLKGAOGPPGPVGIRGDRGAVGVPGFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGLPGFPGAKGEAGFPGTPGVPGYAGEKGDGGLPGLPGRDGLPGADGPVGPPGPSGPQ
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KGMGGLPGFPGLDGQPGGPGAPGLPGAPGAAGPAYRDGFVLVKHSQTTEVPRCPEGQT
                                                                                                                                                                  NDGGNGRPGEPGPPGAPGWDGCNGTDGAPGIPGRPGPPGMPGFPGPPGMDGLKGEPAI
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719. 935
70. 936
70. 936
70. 936
70. 187
991. 1187
70. 1188 . 1250
70. 1260
                                                                                            /db_xref-"SWISS-PROT:P17140"
                              /product="a2(IV) collage
/protein_id="CAA80537.1"
/db_xref="GI:953173"
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/number=11
3924. .3067
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/number=8
3041. .3160
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/number=9
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/number=6
2236. .2735
/number=6
2736. .2911
/number=7
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/number=8
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/number=10
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1725. .2046
/number=5
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/number=7
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/number=4
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/number=9
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join/696. 718,936. 990,1188. 1250,1625. 1724,2047. 2235,

2736. 2911,2963. 3344,3161. 3268,3807. 3923,3970. 4134,

4184. 4455,4503. 5364,5417. 6089,6367. 7181,7227. 7458,

7512. 8303,8386. 8849,8908. 9000)

//note="alternatively spliced transcript"
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IGSIGPKGDPGDLGSVGPPGPPGPREFTGSGSIVGPRGNPGEKGDKGEPGEGGQRGYP
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QKGEAGYPGRDGPKGNSGPPGPPGGGTFNDGAPGPPGLPGRPGNPGPPGTDGYPGAPG
PAGPIGNTGGPGLPGYPGNEGLPGPKGDKGDGGTPGAPGVSGPSGIPGLPGPKGEPGY
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PROFKGBPGVPGMYGTPGMKGLPGLPGDEDSSVPGWKGBRGFNGLPGERGEMSDAA
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GRQGAPGSPGQDGLPGPPGMKGESGYPGQDGLPGRPGLLPGVPGQKGDLGQSGQPGLSG
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AGTPGFPGLKGSPGYPGQDGLPGIPGIRGDSGFPGQPGQEGLPGLSGEKGMGGLPGMP
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KGDLGANGIPGKRGEDGLPGVPGRDGQPGIPGLKGEVGGAGLPGQPGFPGIPGLKGEG
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FKVPESQTLKSGNLRTRVSRCQVCVKSTDGRH"
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NDGGNGRPGEPGPPGAPGWDGCNGTDGAPGIPGRPGPPGMPGFPGPPGMDGLKGEPAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MKQRAALGPVLRLAILALLAVSYVQSQATCRDCSNRGCFCVGEK
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GMGGLPGFPGLDGQPGGPGAPGLPGAPGAAGPAYRDGFVLVKHSQTTEVPRCPEGQTK
Genetic identification, sequence, and alternative splicing of the Ceenorhabditis elegans alpha 2(IV) collagen gene J. Cell Biol. 123 (1), 255-264 (1993) 94012964
                                                                                                           (bases 1 to 9541)
Sibley, M.H.
Sibley, M.H.
Submission
Submitted (15-JUN-1993) Sibley M. H., Northwestern University
Medical School, Cell, Molecular and Structural Biology, 303 E.
Chicago Ave., Chicago, Illinois, USA, 60611
Location/Qualifiers
1. 9541
                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans'
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/protein_id="CAA80536.1"
/db_xref="GI:953172"
/db_xref="SWISS-PROT:P17140"
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/product="a2(IV) collagen"
                                                                                                                                                                                                                                                                                                                     /strain="N2 wild-type"
/db_xref="taxon:6239"
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coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuli Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA aligament program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions, are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                     Submitted (28-JUN-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, Mo 63110, USA 5 (bases 1 to 34671) Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.wormbase.org/db/seq/sequence?name=F01G12;class=Sequence
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                                                                                                                                                                                                                                                                                                                                                                                         st.
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
6 (Dases I to 34671)
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-JUN-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEIGHBORING COSMID INFORMATION
2 (bases 1 to 34671)
Wu, X. and Le, T.T.
The sequence of C. elegans cosmid F01G12
Upublished (2001)
3 (bases 1 to 34671)
                                                                                                                               Direct Submission
Submitted (01-APR-1996) Robert Waterston
4 (bases 1 to 34671)
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                                                                                                                                                                                                                      Direct Submission
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                                                                                                             Waterston, R.
                                                                                                                                                                                               Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998) 99066613 9851916
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 34671)
Waterston, R.
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7182. 7226
/number=16
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6090. .6366
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8304. .838
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PVSTLLTTYCISTAIYSLIRKRQFLLAEGPREFXIDDISSSVKAKNSRLEKVDHVHA
PVSTLLTYCISTAIYSLIRKRQFLLAEGPREFXIDDISSSVKAKNSRLEKVDHVHA
VDQTELTTDEMDPIGTSRSCHNEDVGCCTIFKSTGDV

VDQTELTTDEMDPIGTSRSCHNEDVGCCTIFKSTGDV

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                                                                                                                                                                      6280. 9390
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/note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=F01G12.2a;cla
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LLABGPRERIDDISSSVKAKNSRLEKVDHYHASCEWPQGFTVSLKAYIKVGGTEYGH
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http://www.wormbase.org/db/seq/sequence?name=F01G12.5a.cla
ss=Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="C. elegans LET-2 protein (corresponding sequence F01G12.5b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKQRaaLGPVLRLAILALLAVSYVQSQATCRDCSNRGCFCVGEK
GSMGAPGPQGPPGTQGIRGFPGPEGLAGPKGLKGAQGPPGPVGIKGDRGAVGVPGFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDGGNGRPGEPGPPGAPGNDGCNGTDGAPG IPGRPGPPGMPGFPGPPGMDGLKGEPAI

RAGAPGEKGNOGMPGNPGLPGPSGNDGYPGEKGDRGDTGNAGPRGPPGEAGSPGNPG

IGS1GPRGDPGDIGAMGPAGPPGPIASTMSKGTIIGPRGDLGERGERGEPGEGGORGY

PGNGGLSGQPGLPGMKGEKGLSGPAGPRGKEGRPGNAGPPGFKGDRGLDGLGGIPGLP
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YRGTPGQS1PGLPGKDGKPGLDGAPGRKGENGLPGVRGPPGDSLNGLPGAPGQRGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNGYDGRDGVNGLPGAPGTKGDRGGTCSACAPGTKGEKGLPGYSGQPGPQGDRGLPGM
PGPVGDAGDDGLPGPAGRPGSPGPPGQDGFPGLPGQKGEPTQLTLRPGPPGYPGLKGE
NGFPGQPGVDGLPGPSGPVGPPGAPGYPGEKGDAGLPGLSGKPGQDGLPGLPGNKGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement join (10695. 10787,10846. 11309,11392. 12183, 12237. 12468,12514. 13328,1366. 14278,14331. 15122, 15240. 15511,15561. 15752,515772. 15888,16286. 16396, 166555. 16732,16784. 16959,17461. 17649,17972. 18071, 18446. 18508,18706. 18760,18978. 19000))
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let-2 or clb-1; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                .7442,7904. .8152
                                                                                                                                                                                                                                                                                                                              join(6280. .6441,6487. .6635,7294. .7442,7904. .815
8453. .8622,8942. .9043,9256. .9390)
/gene="F01/G12.2"
/note="coded for by the following C. elegans cDNAs:
yk462h8.3, yk1219b04.3, yk462h8.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="coded for by the following C. elegans cDNAs:
/organism="Caenorhabditis elegans"/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="tRNA-Glu"
complement(10695. .19000)
/gene="let-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id = "AAA96215.1"
                                                                 /db_xref="taxon:6239"
/chromosome="x"
/clone="F01G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:1255877
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/gene="F01G12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F01G12.2"
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                                                                                                                                                                                                                                                                                                                   ss=Sednence"
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gene

CDS

**trna** 

CDS

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/codon_start=1
/product="C. elegans LET-2 protein (corresponding sequence
F01612.5a)"
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                  GAPGLKGGDGLPGLSGQPGYPGEKGDAGLPGVPGREGSPGFPGQDGLPGVPGMKGEDG
LPGLPGVTGLKGDLGAPGQSGAPGLPGAPGYPGMKGNAGIPGVPGFKGDGGLPGLPGL
NGPKGEPGVPGMPGTPGMKGNGGLPGLPGLPGGSGVPGMKGDRGFNGLPGEKGEAGPA
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/db_xref="G1:1255878"
/translation="MKQRAALGPVLRLAILALLAVSYVQSQATCRDCSNRGCFCVGEK
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PKGDVGNPGLPGLNGQKGEPGVGVPGQPGSPGFPGLKGDAGLPGLPGTPGLEGQRGFP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Metazoa; Chordeta; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases i to 123789)
Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="C. elegans collagen alpha 2(IV) chain precursor, let-2 or clb-1; alternatively spliced; coded for by the following C. elegans cDNAs: yk307e10.5, yk339h12.5, yk28618.5, yk274f2.5, yk8098.5, yk274f2.5, yk8098.5, cEES064F, yk479d5.3, yk28488.3, CEESK56FB, yk337c4.3, yk337c4.5, yk443f10.5, yk479d5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAGAAATAAGTGA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AATAACGGCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCACACCCCAGGCCCCC
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.8;
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55.8%;
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Best Local Similarity 55.8
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14084 TGTCGGAAA 14076
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AC110674/c
LOCUS
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VERSION
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SOURCE
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295 GCACCTGGTTTACC 282

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IGTMPLGEKORNG TORANGEROPER TO THE TOTAL THE TO
                                                                                                                                                                                        MMCOLA4 3612 bp mRNA linear ROD 10-FEB-1999 MOLOSE mRNA for basement membrane (type IV) collagen alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See M12879 for genomic exon 14 sequence with differences. Sequence shows interrupted GlyXY nature of collagen alpha chain. Data kindly reviewed (02-SEP-1988) by Wood L. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGPRLSVWLLLLFAALLLHEERSRAPAKGDCGGSGCGKCDCHGV
KGQKGERGLPGLQGVIGFPGMQGPEGPHGPPGQKGDAGEPGLPGTKGTRGPPGAAGYP
GNPGLPGIPGQDGPPGPPGFIPGCNGTKGERGPLGPPGLPGFSGNPGPPGLPGMKGDPG
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OMGSSFQGPKGDKGEQGVSGPPGVPGQAQVKEKGDFAPTGEKKGQKGEPGFPGVPGYGE
KGEPCKQGPRGKPGKDGEKGERGSPGIPGDSGYPGLPGRQGPSGEKGEAGLPGPPGTV
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LKGQPGLPGIPGTPGEKGSIGGPGVPGEQGLTGPPGLQGIRGDPGPPGVQGPAGPPGV
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SGLPGLPGQQGTPGVPGFPGSKGEMGVMGTPGQPGSPGPAGTPGLPGEKGDHGLPGSS
GPRGDPGFKGDKGDVGLPGMPGSMEHVDMGSMKGQKGDQGEKKGQIGPTGDKGSRGDPG
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TPGMPGSPGPRGSPGNIGHPGSPGLPGEKGDKGLPGLDGVPGVKGEAGLPGTPGPTGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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151 >3612
/note="collagen alpha chain precursor (AA -27 to 1127)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (02-SEP-1988)
See M1402 for overlapping sequence (cDNA clone pCIV-1-225, same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae, 1 (bases 46 to 3612)
Wood, L., Theriault, N. and Vogeli, G.
GDNA clones completing the nucleotide and derived amino acid sequence of the alpha 1 chain of basement membrane (type IV) collagen from mouse
                                                                                                                                                                                                                                                                                                 collagen; collagen alpha 1 type IV; collagen type IV. Mus musculus.
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/organism="Mus musculus"

/db_xref="kaxon:10090"

/clone="pcIV-1-PE12, pcIV-1-PE16"

/clone_lib="pys cDNA"

75. 76

/note="uc was cc in [1]"

/inte="uc was cc in [1]"
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/db_xref="SWISS-PROT:P02463"
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/db_xref="G1:50502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 227 (1), 5-8 (1988)
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232. .882
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3338568
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mat_peptide
                                                                                                                                                                                                                             DEFINITION
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JOURNAL
COMMENT
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TITLE
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PUBMED
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                                                                                                                    RESULT 10
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                                                                                                                                                      MMCOLA4
                                                                                                                                                                                                                                                                                                    VERSION
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (14-FEB-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases I to 123789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (18-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Galthersburg, MD 20877, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 123784 bases at least Q40
Consensus quality: 123789 bases at least Q20
Consensus quality: 123789 bases at least Q20
Insert size: 131000; agarose-fp
Insert size: 123789; sum-of-contigs
Quality coverage: 10.94x in Q20 bases; agarose-fp
Quality coverage: 11.58x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is
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Location/Qualifiers
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/note="Genoscope designation: C0AA043116"
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/db_xref="taxon:99883"
/clone="GSTNA-43116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: NISC
Web Site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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Matches 51; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Patent: WO 0188188-A 932 22-NOV-2001;
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/note="helical region (AA 218-1127)"
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Location/Qualifiers
                                                                                                                                                                                                                                                                   37;
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/product="7S protein (AA 1-217)"
232. .276
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                                                                                                                            883. 921
/note="NC2 domain (AA 218-230)"
3475. 3555
/note="exon 4 region"
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Pred. No. 1.7;
0; Mismatches
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AX306181.1 GI:17645461
               232, .276 ... process (AA //Product="N-telopeptide 181
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/organism="Mus musculus"
/db_xref="taxon:10090"
a 1798 c 1950 g 121:
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/citation=[1]
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61.5%;
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GPGSPGLPGPKGEAGKVVPLPGPPGAAGLPGSPGFPGPQGDRGFPGTPGRPGIPGEKG
AVGDPGIGFPGLPGPKGVDGLPGEIGRPGSPCRPRGFNGLPGPPGQCKGEPGIGLPG
LKGQPGLPGTPGEKGSIGGPGVPGBGLTGPPGLQGIRGDPGPPGVQBPGVPGV
PGIGPPGAMGPPGGEPPGSSGRGPGFPGLLDMPGPRGDKGSQGLPGLTG
SGLPGLPGQQGTPGVPGPGSKGEMGVMGTPCQPGSPPGPTPGLLPGSQGLPGLTGS
GERGDPGFKGDNGCPPGSKGEMGVMGTPCQPGSPGPAGTPGLPGSKGDHLPGSS
GBRGDPGFKGDNGLPGMPGSMEHVDMGSMKGQKGDQGFKGQIGPTGDKGSRGDPG
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RKSTWPFLECHNINWVCNFASNDVSYWLSPPEDRMSMAPH SEGNNIFFEISRCAVCE
RAPANWANHSQTIQTPQCPNGWSSIMJGSSWWHTSAGESSGQALASPGSCLEEFRS
APFIECHGRGTCNYYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMRR
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GNPGLPGIPGQDGPPGPPGIPGCNGTKGERGPLGPPGLPGFSGNPGPPGLPGMKGDPG
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TPGMPGSPGPRGSPGNTGHPGSPGLPGEKGDKGLPGLDGVPGVKGEAGLPGTPGPTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"alpha-1 type IV collagen"
/protein_id="AAA50292.1"
/db_xref="GI:556297"
/translation="MGPRLSVWLLLLPAALLHEERSRAAAKGDCGGSGCGKCDCHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMGSSFQGPKGDKGEQGVSGPPGVPGQAQVKEKGDFAPTGEKGQKGEPGFPGVPGYGE
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EGLPGPQGSPGLIGQPGAKGEPGEIFFDMRLKGDKGDPGFPGQPGMPGRAGTPGRDGH
PGLPGPKGSPGSIGLKGERGPPGGVGFPGSRGDIGPPGPPGVGPIGPVGEKGQAGFPG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 6512)
Muthukumaran,G.; Blumberg,B. and Kurkinen,M.
Muthukumaran,G.; Blumberg,B. and Kurkinen,M.
The complete primary structure for the alpha 1-chain of mouse collagen IV. Differential evolution of collagen IV domains J. Blol. Chem. 264 (11), 6310-6317 (1989)
89197932
2703490
On Oct 8, 1994 this sequence version replaced gi:340547.
                                                                                                                                                                                                                                                                                                                                         8, 1994 this sequence version replaced g1:340547.
Location/Qualifiers
1. .6512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type IV collagen"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="parietal endodoerm"
/dev_xfage="13.5 day old embryo"
1. .6512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132. .212
/gene="Col4a-1"
213. .5138
/gene="Col4a-1"
/product="alpha-1 t;
5406. .5411
/gene="Col4a-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative"
5765. .5770
/gene="Col4a-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .014a-1"
/note="putative"
5777. 5700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132. .5141
/gene="Co14a-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="putative"
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/gene="Col4a-1"
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g δ QQ

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/codon_start=1
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Hydra sp.
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ORGANISM
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TITLE
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TITLE
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GPPGLPGLPGPHGPRGLAGLPGCNGSKGEQGFPGFPGTPGTPGLTGCPKG
GPPGLPGLPGPPGPPGPPGFPGPGPGPGPPGPPGFPGLPGPAGPRGPRGPKGPKGPM
GDBNGFRGCPPGTPPGFPGFPTTTTOPYNKSDFKGERGDBGERGEPGPPGPS
GPPGDSTGGKGERGMCATGPPGPPGTYUFTTTOPYNKSDFKGERGDBGGERGEPGPPGPS
GPPGDSTGSEKGAPGEPGPRGKPGKDGPGPFGTEGAKGNRGFPGLRGEAGIKGRKGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF169387 7765 bp mRNA linear ROD 16-NOV-1999 Mus musculus alpha 3 collagen IV (Col4a3) mRNA, complete cds.
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PIGWPGLKGSKGERGPPGKDTVGPPGPLGCPGSPGPPGPPGPPGPPGDTVFKCSPGEH
GWPGDTGPPGVPGLDGPKGEPGSPCTECHCFPGPPGVPGFFGLDGIKGIPGGRGVPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGNPGSPGSAGLPGFAGFPGDQGHPGLKGDKGDTPLPWGQVGNPGDPGLRGLPGRKGF
DGTPGGPGAKGPPGPQGEPALSGRKGDQGPPGFPGPPGPPGPAGPAGPAGPGYGPQGEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MHSKTAPRFLVFLLLTLLLLAASPVASKGCVCKGKGQCLCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. Lu.W., Phillips.C.L., Killen, P.D., Hlaing, T., Harrison, W.R., Elder, F.F., Miner, J.H., Overbeek, P.A. and Meisler, M.H. Insertional mutation of the collagen genes Col4a3 and Col4a4 in a mouse model of Alport syndrome Genomics 61 (2), 113-124 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-JUL-1999) Department of Pathology, Box 0602, University of Michigan, 1301 Catherine, Ann Arbor, MI 48109-0602, USA
                                                                                                                                                                                                                                                                            2692 CAGGACAGTCAGGCCTCCCTGGCCTTCCTGGACAGCGGGACACCTGGACATCCAGGGT 2751
                                                                                                                                                                                                                                                     53 CTGGACCTCCAGCACCCCCAGGGCCCCCAGAAGAAGTGGGGGCCTCCTGGTGCACCAGGTT 112
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lu,W., Phillips,C.L., Killen,P.D., Hlaing,T., Harrison,W.R., Elder,F.B., Miner,J.H., Overbeek,P.A. and Meisler,M.H. Direct Submission Submitted (15-JUL-1999) Department of Pathalogue.
                                                                                                                                                                                                                   ;
                                                                                                                                                                            Length 6512;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                 37;
                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                    2752 rcccaggrrcraaaggrgaargggrgrcargggaa 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="alpha 3 collagen IV"
/protein_id="AAD50449.1"
/db_xref="GI:5739385"
                                                                                                                                                                                                                                                                                                                                   113 TACCACAATATACAGGAGAAATAAGTGAAATGACAA 148
                                                                                                                                                                        Score 36.8; DE
Pred. No. 1.8;
0; Mismatches
                                                                                                                1211 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="embryonic"
1. .7765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .7765
                                                                                                                    Б
              5858. .5863
/gene="Col4a-1"
/note="putative"
6512
                                                                                            /gene="Col4a-1"
1798 c 1950
'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Col4a3"
370. .5379
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/gene="Col4a3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF169387.1 GI:5739384
                                                                                                                                                                        23.7%;
61.5%;
                                                                                                                                                                                                                 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
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                  polyA_signal
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AF169387
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GAKGSPGRCIPGPRGTQGLPGLNGLKGQPGRRGDTGPKGDPGIPGMDRSGVPGDPGPP
GTPGCPGEMGPPGQKGYPGAPGFPGPPGEKGEVGMMGYPGTTGPPGLPGRPGSQQGRG
SLGIPGMKGEKGRPGARGKGKPGPPSQTTLLKGDKGEPGLKGFVGNPGEKGNRGN
PGLPQPRGLEGLPPGLPGPPGDTGSRGNPGRPGPHGMPGSMGIMGYPGPKGRKGTS
                                                                                                                                             PGQSGPAGPDGAPGSPGSPGHPGKPGPAGDLGLKGQKGFPGPPGSTGPPGPPGLPGLP
GPMGMRGDQGRDGIPGPPGEKGETGLLGAYPGPKGSPGVPGAKGDRGVPGLSGLPGRK
GVMGDVGPQGPPGTAGLPGPPGLPGAIIPGPKGDRGLPGLRGNPGEPGPPGPPGPIGK
                                                                                                                                                                                                                                                                                          PGIPGPCGPRCKPGKDGKPGTPGPAGTKGNKGLKGQQGPPGLDGLPGLKGNPGDRGTP
ATGTRANGFIFTRHSQTTA.IPSCPEGTQPLYSGFSLLFVQGNKRAHGQDLGTLGSCLQ
RFTTMPPLECKINNVCNFSRNDYSYMSTPALMPMDMAPISGRALEPY ISRCTVCEG
PRATA AVHSQTTA.IPSCPCQDWSTSWSTSTPLTAGESGFGAGGALASPGSCLEFFRAS
PFIECHGRGTCNYYSNSYSFWLASLMYGFSFTPTTAGTAGDLGKIISRCQVCMKKR
                                                                                                                 GLPGLAGRPGRTGIHGPQGDKGEPGYSEGARPGPPGPKGDPGLPGDKGKKGERGVPGP
                                                                                                                                                                                                                                  GIKGDKGFMGPPGPKGLPGTVGDMGPPGFPGAPGTPGLPGVRGDPGFPGFPGIKGEKG
NPGFLGPIGHPGPVGPKGPPGPRGKPGTLKVISLPGSPGPPGVPGQPGWKGDPGPLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eŭkaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 ATCAGGGGAATAACTGGATTACCAGGGTTTGCAGGTCCTCCTGGACTTCCAGGCCTCCCA 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GAAGAAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAATATACAGGAAAATAAGTGAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ATAACGCCAGTCATTGAGCATGTAGAAGTTGCTGGACCTCCAGCCACCCCCAGGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 GGCCACCCTGGGCTGGCTGTTTACCAGGATGCAAAGGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Score 36.8; DB 10; Length 7765; 56.7%; Pred. No. 1.9; tive 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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/clone_lib="lambda gt10, I-cellspec."
14. .676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X61045.1 GI:9446 collagen homologue; N-COL 1 gene; nematocyst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydra N-COL 1 mRNA for mini-collagen.
X61045 S66747
X61045.1 GI:9446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="N-COL 1"
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Ractus.

Ractus.

Ractus.

Rababara, J. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Rabbara, J., Banton, J., Binge, K., Blankenburg, K., Bonnin, D.,

Bunck, J., Benton, J., Binge, K., Blankenburg, K., Bonnin, D.,

Bunck, J., Benton, J., Binge, K., Blankenburg, K., Bonnin, D.,

Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavacos, S.R., Chace, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Chen, G., Chen, R., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Davila, M.L., Davis, C., Davy Carroll, L., Dederich, D.A.,

Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,

Douthwalte, K.J., Draper, H., Dugan Rocha, S., Durblin, K.J.,

Earnhatt, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,

Gorrell, J.H., Guevara, M., Garner, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, M., Hogues, M., Holloway, C., Hollins, B.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Karlscon, E., Kelly, S., Khan, U., King, L., Kovar, C., Lewis, L.,

Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,

Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Lune, M., Mattinez, E.,

Maheshwari, M., Mavhiney, E., Martinez, R., Martinez, E.,

Maneshwari, M., Mavelby, P., Marting, M., Morris, S.,

Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M.,

Miner, G., Miner, S., Mitchell, T., Mohabbat, K., Morgan, M.,

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Rassey, E., Mavhiney, E., Mitchell, T., Mohabbat, K., Morgan, M.,

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Mares, M., Marten, M., Marten, M., Mersey, M.,

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Mares, 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note-"proline repeat"
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                                                                                                /db_xref="SPTREMBL:Q00484"
/product~"mini-collagen"
/protein_id="CAA43379.1"
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Nguyen, N. Nickerson, NewLabon, N. Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraqunye, N., Ovledo, R., Parken, B., Oguh, M., Okwuonu, G., Oraqunye, N., Ovledo, R., Parmus, E., Pu, L.L., Quiles, M. Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolle, M., Rultz, S., Savery, G., Scherer, S., Scott, G., Shan, H., Shooshtari, N., Sisson, I., Sutton, A., Svattek, A., Tabor, P., Tamerisa, R., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Wang, G., Walliams, G., Warren, R., Washington, C., Warlington, S., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Weistcock, G. and Gibbs, R., Wallia, S., Nelson, D., Unpublished
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NOTE: This is a "working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
Submisted (11.7UL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced g1:17943819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 95492)
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Contact: hgsc-help@bcm.tmc.edu
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23.6%; Score 36.6; DB 2;
Best Local Similarity 58.9%; Pred. No. 2.7;
Matches 63; Conservative 0; Mismatches 44;
Location/Qualifiers
1. .95492
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/db_xref="taxon:10116"
/clone="CH230-11E5"
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 2615)

S Lu,X., Cui,L. and Li,Y.

DDRT-PCR from B cell

AL Unpublished (2000)

Contact: xingwu Lu,liangxian Cui,yonghal Li

Department of Biochemistry

Institute of Basic Medical Science, Peking Union Medical College

Dongban SanTiao 5, Beijing, P.R.C, 100005

Tel: 86-010-65296951

Email: luxingwu@263.net

full-length and coding sequence.

S Location/Qualifiers
                                           ACO064124 Pan trog1
BMS54723 AGENCOURT
ACO064124 Pan trog1
BM926985 AGENCOURT
ACI12666 Pan trog1
BC422247 AGENCOURT
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ACO16929 BPN trog1
ACO16239 PAN trog1
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ACO15299 BPN trog1
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ACO1239 HOMO SAPI
ACO13644 PAN TROG1
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32-393 human bone marrow cDNA library Homo sapiens cDNA, mRNA
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/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EBCORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5 adaptor: GGCAGAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, BerKeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                              41;
                                                                                                                                   Length 2615;
                                                                                                                                                              Indels
                                                                                                                 Score 675.4; DB 10.
                                                                                                                                    DB 10;
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0; Mismatches
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11 Similarity 80.5%;
856; Conservative
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 14 Row: d Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12 MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                 AGTTTCATAAGGGAGGCAGAGCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATA 510
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                                                                                                                                                                                                                                                                                                              Homo sapiens, Similar to hypothetical protein FLJ14058, clone
IMAGE:3831313, mRNA.
                  CACTGGATTTCGGACTTATATGGGGCCCGTA-CCCCTTTGTTTTGGCCAATTTTTCCAT
CCTGGACGTGAGACATGGAGTCAAAAGAGATCATTTTGGAGCTTTAAAGATTTGACTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone has the following problem: frame shifted
                                                                                                                                                                                                                                                                                                linear
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/lab_host="DH10B-R"
                                                                                                                                                          TIGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTGTAT 1376
                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
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llarity 78.2%; Pred. No. 1.9e-170;
Conservative 0; Mismatches 205;
                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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513 g :
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Primates;
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BC004496.1 GI:14709139
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Strausberg,R.
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Matches 781;
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ORIGIN
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AUTHORS
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SOURCE
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Euteleostomi;

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="human B lymphocyte cDNA library"
/tissue_type="bone marrow"
/note="Organ: tongue; Vector: pAMP10; mRNA made from
/note="Organ: tongue; Vector: pAMP10; mRNA made from
/note="Organ: conge into UGC sites. Size-selected on
agarose gel, average insert size 500 bp. Primary library.
CDNA Library Preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research
                                         Lu,X., Cul,L. and Li,Y.
DDRT-PCR from B cell
Unpublished (2000)
Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking Union Medical College
Dongban SanTiao 5, Beijing, P.R.C, 100005
Tel: 86-010-65296951
Email: luxingwu2663.net
full cDNA sequence.
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              Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                       Length 1514;
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                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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Pred. No. 1.8e-158;
0; Mismatches 131;
             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1514)
                                                                                                                                                                               Location/Qualifiers
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81.0%;
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Best Local S
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 ORGANISM
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ORIGIN
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AUTHORS
TITLE
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GGGAC------AGGCCCAGGGTCCCTGTGCTGTGCAGCCTAGAGACTTGGTGCC
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                                                  GAGAAGAAAAGCCCATTTTTGAGGAGAAATTCAAGCCAGCTGCATAAATTTGCATAAGT
                                                                                      AATGAGGAGCTGAATGTTAATCCTCAAGACAATGGGGAAAATATCTCCTGGACATGTCAG
                                                                                                  CTGTGTCCCAGTTAA - - TTCAGCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTTGGCAG
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                                     AACTGCCGTATTTACCCAATGCCTGTACCTCCATTGTAT 1376
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//Issue_type="malanoitc melanoma"
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//Issue_ty
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MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: GapbS-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.g column: 18
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Pred. No. 9.5e-131;
0; Mismatches 150;
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BI488505 870 bp mRNA linear EST 28-AUG-2001 603021014F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191803 5',
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Vakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          CTAGGAG---AAAATGGTTTTGTGGGACAGGCCCAGGGTCCCTGTGCTGTGTGCAGCCTA
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BI488505.1 GI:15327733
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553 GCAGAAATTTGCATATGTAATGAGGAGCT--GAATGTTAATCCTCAAGACAATGGGGAAA 610

Matches

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/note="Organ: Drain; Vector: pCNV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for [Inli-length clones and was constructed by C. Gruber (Inli-length). Research Genetics tracking code 019. Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMI479 row: k column: 04
High quality Sequence stop: 849.
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  NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.3e-130;
0; Mismatches 168; Indels 35;
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/clone="IMAGE:5191803"
/clone_lib="NIH_MGC_114"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Best Local Similarity 76.1%;
Matches 645; Conservative (
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Best Local
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/db_xref="taxon:9606"
/clone="InMcE:5583427"
/clone="InMcE:5583427"
/clone="InmcE:5583427"
/tlssue_type="embryonal carcinoma, cell line"
/tlssue_type="embryonal carcinoma, cell line"
/tlssue_type="embryonal carcinoma, cell line"
/tlssue_type="embryonal carcinoma, cell line"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
http://sequence.comm: 20
High quality sequence start: 9
High quality sequence stop: 713.
CCAGTGGGGCTCCATCTAGTAGAGCTGTGAGAAGAAGTCCACCACCTCCAGACTCCAGA 1057
                                                                                                                                                                                                                                                                             AGCCTGTGAAAGCAGCAGGGATGGAGTCTGTACCCTACAAAACCGTAGTGGCAGAGCTGA 1177
                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGACCTGGACGTGAGACATGGAGTCA 1237
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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228 c 254 g 191 t
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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5'-TCGACCCAGGGTCGG-3' and 5'-TCGACCCAGGGGCGCCCT(15)-3' Size selected > 5'-GACTAGTTCTAGATCGCGAGCGGCGCCCT(15)-3' Size selected > 1' Ab for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
          NITH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMA1360 row: c column: 16

High quality sequence stop: 722.
                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_2: Sal1; cDNA made by oligo-dr priming. Directionally cloned using the following adaptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 AAGAAAACCCATTTTCTGAGGGGAAATTCAAGCTGGCTGCAGAAATTTGCATATGTAAT 573
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                                                                                                                                                                                                                                                                                                                         /clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 469.8; DB 14;
Pred. No. 1.4e-127;
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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6179271"
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ilarity 75.48;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                               ACATGTCAGAGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGCCTAGGAG---A
                                                                                AAATGGTTTTGTGGGACAGGCCCAGGGTCCCTGTGCTGTGTGCAGCCTAGAGACTTGGTG
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                  35 TGCATAAGCAGCAAGGAGCCTAATGTTAATCCCCAAGACCATGGGGAAATGTCTCCAGG
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BQ723415 941 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8305155 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6193072 5', mRNA sequence.
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                                                Length 1050;
                                                                                Indels
                                               Score 462.6; DB 13;
Pred. No. 2e-125;
0; Mismatches 199;
221
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272
                                               33.6%;
74.8%;
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                                                              Best Local Similarity 74.8
Matches 638; Conservative
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Homo sapiens CDNA clone IMAGE:5539381
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I (bases 1 to 1050)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DATP
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/clone="IMAGE:5539381"
/clone="IMAGE:5539381"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
                                                                                1071
            GTAGTACAAAAGGGAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCA 1011
                                                                                                                                               1072 GACAGCTTGCAGCATGTGCCTGAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCA 1131
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                                                                                                   /organism⇒"Homo sapiens"
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AUTHORS
TITLE
JOURNAL
COMMENT
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 876)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP

CONTACT: RObert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov.

Location/Qualifiers

Location/Qualifiers
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/clone_lib="NHH_MGC_72"
/tissue_type="melanotic realsoms"
/lab host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                  591 GGATGCCCAGAGAAGTTTGTTGCAGGGACAGGGCCCTCATGGAGAACTTCTGCTAGAG
                                                                                                                                                                                                                                                                                                                     953 TAGTACAAAAGGGAAATGTTGGGTGGGAGCCCCCCACAGAGTCCCCAGTGGGGCTC-CA
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                                       11 TCCCAGCTGCTCCAGCTGTGGCTGAAAGGGGCTATCACAGAGCTCAGGCTGTGGCTTCAG
                                                                              AGGGTGCAAGCCCTAGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGA
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/db_xref="taxon:9606"
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NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACACCGTCGG-3' and
5'-GACTAGTTCTAGATCGCGAGCGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠.
م
                                                                                                                                                                                           Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabar-femail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LiaMi3596 row: b column: 17
High quality sequence stop: 606.
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 94). NIH-WGC http://mgc.nci.nih.gov/. NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:6193072"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 451.4; DB 14;
Pred. No. 4.1e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .941
/organism="Homo sapiens"
/db_xref="taxon:9606"
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78.0%;
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                                                                                Homo sapiens
  BQ723415
BQ723415.1
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Lotoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submitssion
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC):
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RsD process and may have higher chance of
   Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1164
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                                           Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Male BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 430.4; DB 17;
Pred. No. 6.1e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 106;

    717
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
    /clone="PTB-085H08.F"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="PTB Chimpanzee
189 c 195 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                                   Sequencing: -21M13
                                                                                                                                                                                                                                                                     clone tracking errors.
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82.4%;
                                                                                                      (bases 1 to 717)
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Pan troglodytes
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 ctionally. Primer: Oligo dT
Library constructed by Life
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                                                                                                                                                                                                         452 GTTTCATAAGGGAGGCAGAGCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATAA 511
                                                                                                                                                392 AAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTCA 451
                                                                                                                     Gaps
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                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876;
                                                                                      Score 435.6; DB 14; Length
Pred. No. 1.9e-117;
0; Mismatches 120; Indels
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Site_2: Sall; Cloned unidirectionally.
Average insert size 2 kb. Library con
Technologies "
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AG086951
AG086951.1 GI:16638753
                           Technologies.
                                                                                      31.6%;
78.9%;
                                                                                                                    Conservative
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                                                                                                                    Matches 610;
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AG086951
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Chases I to 676)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:si81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGU64424 676 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-053H24.R, genomic survey sequence.
AG064424
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Pan troglodytes
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
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/db_xref="taxon:9666"
/db_xref="Inaxon:9666"
/clone=lib="Inage:5468441"
/clone_lib="MiH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/tissue_type="amelanotic melanoma, cell line"
/tab_host="DHLOB (phage-resistant)"
/note="Organ: skin; Vector: poTP3; Site_l: XhoI; Site_2:
FOORI; CDNA made by Oilgo-dT priming, Directionally cloned
into Ecorl/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases I to 1076)

NIH-MGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1973 row* b column: 11

High quality sequence stop: 665.
                                                                                                                                                                                                                                                                                                                          BM554723 1076 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6578521 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468842
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Contact: Robert Strausberg, Ph.D.
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AGENCOURT_6681877 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767880
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480
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                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                182 GTATGGAAATGCCTGGATGTCCAGGCAGAAGTTTGCCGCAGGGACGGGGTCCTCTTGGAG
                                                                                                                                                                          AGCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTTGGCAGCTTCCAAGTGGTGTTGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        819 TGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGAT
                                                                                                                                                                                                                                              122 GGCAAGTGCACAGAAGTCAAGAACTGGGGTTTAGGAACCTCTACCTAGATTTCAGAGGAT
                                                                                                                                                                                                                                                                     601 GCCTGTAGCCCCTTTGTTTTGGCCAATTTCTCCCATTTGGAATGGCTGTATTTACCCCAAT
                                                                                                                                                                                                                                                                                                                   ;
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                                                                     /clone_lib="PTB Chimpanzee Male BAC Library"
165 c 191 q 156 +
                                                                                                                              Length
                                                                                                                                                     Indels
                                                                                                                            Score 419.8; DB 17;
Pred. No. 8.2e-113;
0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-053H24,R"
Location/Qualifiers
1. .676
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                                                                                                                            Match 30.5%;
Local Similarity 82.3%;
les 506; Conservative
                                                          /sex="male"
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//note-Torgan: Drain: Vector: pCWV-SPORT6; Site_1: NOLI; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIHGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                          Email: cgapbs remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and through the I.M.A.G.E. Consortium/LLNL at:
http://imag.lln.gov
Plate: LLAM12826 row: n column: 09
High quality sequence stop: 613.
Location/Qualifiers
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Pred. No. 9.8e-112;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:5767880"
/clone_lib="NIH_MGC_121"
/lab_host="DH108"
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completed: February 20, 2003, 06:15:08
ne : 3510.23 secs
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                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1080)
NH-MCC http://mgc.nol.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Lissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally; oliqo-dT primed.
Average insert size 2.5 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
1304 -TACCCCTTTGTTTTGCCCAATTTTTCCATTTGGAACTGCCGTATTTACCCAATGCCTG 1362
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13211 row: o column: 15
High quality sequence stop: 702.
Location/Qualifiers
                 390 GGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATT 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6015590"
/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                                                                        BQ422247.1 GI:21117562
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                                                                 1363 TACCTCCATTGTAT 1376
                                                                                       669 TACCCCCATGTAT 682
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AGAGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGGCCT - - - AGGAGAAAATGGT
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61 CCAGCACACCCCAGGCCCCCAGAAGAGTGGGGCCTCCTGGTGCACCAGGTTTACCACAA 120
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APPLICANT: FOX, Brian
APPLICANT: HOLLOway, James L.
TITLE OF INVENTION: ZACRPI3
TITLE OF INVENTION: ZACRPI3
TITLE REPERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT APPLICATION NUMBER: US/09/997,610
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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US-09-997-610-1
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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US-10-038-806-6
US-10-003-806-6
US-10-003-806-9
US-09-835-232-7
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US-10-003-806-6
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DB 9; Length 1381; Indels

100.0%; Score 1377; 100.0%; Pred. No. 0; iive 0; Mismatches

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Sequence 1, Appii
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Sequence 2765, Ap
Sequence 2765, Ap
Sequence 2761, Ap
Sequence 1543, Ap
Sequence 2298, Ap
Sequence 2764, Ap
Sequence 2793, Ap
Sequence 3, Appii
Sequence 6644, Ap
Sequence 6752, Ap
Sequence 6754, Ap
  Sequence 316,
Sequence 1, Ap
0 US-09-967-768A-316

0 US-09-768-877-1

0 US-09-764-877-1

0 US-09-764-877-2791

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GENERAL INFORMATION:
APPLICANT: Fox, Brian
APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE CO
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
                                                                                                                                                                                                                                        100.0%;
100.0%;
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Matches 1377; Conservative
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US-09-997-610-5
                                                                                                                                                                                                            NAME/KEY: CDS
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Pred. No. 0;
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CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                        Sequence 5, Application US/09997610 Patent No. US20020156244A1
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ORGANISM: Artificial Sequence
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APPLICANT: Holloway, James L.
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELAY:
TITLE OF INVENTION: ACRP13
FILE REFERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/253,924
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 3
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Patent No. US20020156244A1
GENERAL INFORMATION:
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OTHER INFORMATION: Degenerate polynucleotide OTHER INFORMATION: of SEQ ID NO:2 NAME/KEY: variation LOCATION: (1)...(1377)
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                  OTHER INFORMATION: Each n is independently NAME/KEY: misc_feature LOCATION: (1)...(1377)
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OTHER INFORMATION: n =
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Patent No. US200201562441
GENERAL INFORMATION:
APPLICANT: FOX. Brian
APPLICANT: FOX. Brian
TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PRO;
TITLE OF INVENTION: ZACRP13
FILE REFERENCE: 00-96
CURRENT APPLICATION NUMBER: US/09/997,610
CURRENT ELLING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1
OTHER INFORMATION: containing KvLQT1 gene)
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APPLICANT: Zuker, Charles S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: Ion Channel
FILE REFRENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/259,379
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 6
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Pred. No. 3e-182;
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Patent No. US20020164645A1
GENERAL INFORMATION:
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                                                   GGGTGCAAGCCCCAAGCCTTGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAA
                                                                                                                      GTCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTG
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CURRENT APPLICATION NUMBER: US/09/933,267A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/16026

PRIOR APPLICATION NUMBER: 60/18356

PRIOR FILING DATE: 1999-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2001-03

PRIOR FILING DATE: 2001-03-34

PRIOR FILING DATE: 2001-03-44

PRIOR APPLICATION NUMBER: 09/804076

PRIOR APPLICATION NUMBER: 09/804076

PRIOR APPLICATION NUMBER: 09/804076

PRIOR FILING DATE: 2001-03-13

PRIOR FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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; Patent No. US20020113095A1
; APPLICANT: Kalush, Francis et al.
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TAT 439809
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; ORGANISM: Human
US-10-003-806-6
                                                                                           TAT 1376
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                                                             Length 465237;
                                                                                 Indels
                                                          Score 618.2; DB 10;
Pred. No. 6.6e-175;
0; Mismatches 193;
                                                         Query Match
Best Local Similarity 78.2%;
Matches 847; Conservative
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                   TYPE: DNA
ORGANISM: human
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                                       US-09-933-267A-1
SEQ ID NO 1
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                           439687 GCTITAGAAITIGACTGCCCTGGTGGATTITAGACTTGTGTGGGCCCTGTAACCCCTTTG
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APPLICANT: Bishop, Colin E.
APPLICANT: Bishop, Colin E.
APPLICANT: Agoulnik, Alexander I.
TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P02066US1/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
CURRENT FILING DATE: 20001-11-02
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR PILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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78.9%; Pred. No. 9.8e-173;
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Patent No. US20020119929A1
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Matches 809; Conservative
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123192 GATGCCCAGGCAGAAGTTTGCTGCAGGGGTGGGGCCCTCATGGAGAACCTCTGTTAGGAC 123251
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APPLICANT: Bishop, Colin E.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: About Grand
TITLE OF INVENTION: Can 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P02066US1/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
CURRENT FILING DATE: 2000-111-03
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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78.9%; Pred. No. 9.8e-173;
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Patent No. US20020119929A1
GENERAL INFORMATION:
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Matches 809; Conservative
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ORGANISM: Human
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Patent No. US20020098489A1
GENERAL INFORMATION:
APPLICANT: Leder, Philip
APPLICANT: Leader, Benjamin
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US-09-734-674-3/c
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                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 1.1e-170;
0; Mismatches 166;
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; OTHER INFORMATION: n= A,T,C, or
US-09-835-232-7
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.6%;
Matches 816; Conservative
                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                LENGTH: 170834
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Sequence 3, Application US/09734674

Patent No. US20020081648A1

GENERAL INFORMATION:

APPLICANT: WEI, MISCHAID HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOOlolla

CURRENT APPLICATION NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 202001
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                                               GGATGGAGTCTGTACCCTACAAAQCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCT
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Pred. No. 1e-166;
0; Mismatches 171; Indels
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OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 78.4%;
Matches 803; Conservative
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Db 560894 GAACTTTGAACTTGAGAGATGATTTAGCGTATCTGGCAGAAATTTCTAAGCAGCA 560835
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Pred. No. 2.3e-155;
0; Mismatches 217;
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NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                   US/09/263,959
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684973 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.4%;
Matches 797; Conservative
                                05-MAR-1999
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 TTCAGAGGG------
                     APPLICATION NUMBER
                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-09-263-959-1
                                  FILING DATE: 0 CLASSIFICATION:
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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39727 TCTCAGTCAGGCACAGGGTACCCATCCTGTATACAGCCTAGGGACTTGGTGCCCTGTGTT 39668
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                                                                                           GGTGCAAGCCCAAGCCTTGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAG
                                                                                                                                                           TCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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COUNTRY: US
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28480 GGTIGGAGCCTICACACAGAGICCCCACIGGAGCACIGCCIAGIGGAGCTGTGAAAAGAG 28421
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Publication No. US20030022337A1
Publication No. US20030022337A1
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND UTITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND UTITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01078
CURRENT APPLICATION NUMBER: US/09/819,607
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 5
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                                                     CTGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGTAGTACAAAAGGGAAATGTTG
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                                  GGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTTGGG
                                                                                                    AACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTG
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CTAAAAGGAGCCAAGGTACAGCTCAGGCCATGGCTTCAGAAGGTGCAAGCCCCAAGCCCCT
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4.4e-147;
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US-09-819-607-3/c
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Matches 69
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Patent No. US20020115136A1

GENERAL INFORMATION:

APPLICANT: WERKULOW et al.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOOL103

CURRENT APPLICATION NUMBER: US/09/777,921A

CURRENT PILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 126

SOGTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30.00
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                                                                                                    GTAGTGGCACAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGACCTGGAC
                                                                                                                                                                        GTGAGACATGGAGTCAAAAGAGATCATTTTGGAGCTTTAAGATTTGACTGCCCCACTGGA
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 TCCTCCAGACCCCCAGAATGGTAGATCCACCAACAACTTGTGCTGTGTACTTGGAAAAGCC
                                  ACAGACACTCAGTGCCAGCCTGTGAAAGCAGCAGGGATGGAGTCTGTACCCTACAAAACC
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Pred. No. 2.4e-153;
0; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.6%;
Best Local Similarity 77.0%;
Matches 727; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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N: EXPRESSED IN PLACENTA, SIGNAL = 20
N: EXPRESSED IN BRAIN, SIGNAL = 14
N: EXPRESSED IN HBLIA, SIGNAL = 15
N: EXPRESSED IN HBLIOO, SIGNAL = 12
N: EXPRESSED IN HBART, SIGNAL = 12
N: EXPRESSED IN BY 74, SIGNAL = 12
N: EXPRESSED IN FETAL LIVER, SIGNAL = 14
N: EXPRESSED IN FETAL LIVER, SIGNAL = 14
N: EXPRESSED IN LUNG, SIGNAL = 14
N: EXPRESSED IN BONE MARROW, SIGNAL = 14
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-20
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-06-08
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-09-04
PRIOR PELING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DA
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OTHER INFORMATION: E
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INFORMATION:
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ORGANISM: HOMO
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LENGTH: 1946
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Patent NO. US20020048763A1
CENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                           14264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14563 AGCAACAAGGAACTGAATATTAATCACCAAGACAATGGGGAAAATGTCTCCAGGGCATGC 14504
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Publication No. US20030027307A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001160DIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
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                                                                                                  FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(148567)

US-10-254-869-3
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Matches 781; Conservative
SOFTWARE: FastSEQ fc
SEQ ID NO 3
LENGTH: 148567
TYPE: DNA
ORGANISM: Human
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Patent No. 5171840
Patent No. 5480796
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Sequence 3,
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                              February 19, 2003, 16:09:30; Search
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US-09-146-053-5

US-08-991-789A-29

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US-09-68-76-12

US-09-68-76-12

US-08-687-080-59

US-08-687-080-59

US-09-463-911-6

US-09-140-804-9

US-09-140-804-1

US-09-336-536-1

US-09-336-536-1

US-09-336-536-1

US-09-336-536-1

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US-09-439-856-3
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Listing first 45 summaries
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APPLICANT: HOUNSKY, KENNETH S.
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: SREENAN, SEAWUS
APPLICANT: SREENAN, SEAWUS
APPLICANT: APPLICANT: OTANI, KENICHI
APPLICANT: APPLICANT: OTANI, KENICHI
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
APPLICANT: BILL, GRAEME I.
APPLICANT: BILL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 300
SOFTWARE PETENT VET. 2.0
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Pred. No. 1.1e-129;
0; Mismatches 204;
                         US-08-795-473B-2
US-09-439-856-2
US-09-415-551-1
US-09-065-474-136
US-09-557-034-136
US-09-557-034-136
US-09-557-034-137
US-09-449-218D-1
US-09-449-218D-1
US-09-449-218D-7
US-09-449-218D-18
US-08-640-386A-3
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Patent No. 6235481
GENERAL INFORMATION:
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72.0%;
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ORGANISM: Human
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                            TGGTGCCCTGTGTCCCCAGTTAATTCAGCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTT
                                                                                      794 GGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGG
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Pred. No. 1.8e-79;
0; Mismatches 332;
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US-09-146-053-5
Sequence 5. Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gen.
FILE REFERENCE: MCG103
CURRENT FILING DATE: 1998-09-02
ERALIER FILING DATE: 1998-09-02
ERALIER FILING DATE: 1997-09-02
MUMBER OF SEQ ID NOS: 7
                                                        47677 TGGTGCCCACATCCCAG-------
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62.2%;
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Best Local Similarity 62.2
Matches 585; Conservative
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US-09-146-053-5
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Human RAD50 Gene and Methods of Use Thereof
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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1004 GGGCTCCATCTAGTAGAGCTGTGAGAAGTCCACCATCCTCCAGACTCCAGAAGGGTA 1063
                                                                                                                                                                                                                                           APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 247.4; DB 4;
Pred. No. 3e-69;
0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                     Sequence 29, Application US/08991789A Patent No. 6225054 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
2.P: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                         14378 CCTGTATCCCCATTGTAT 14361
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68.6%;
                                                       1359 CCTGTACCTCCATTGTAT 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
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                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
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                                                                                                                                                   RESULT 4
US-08-991-789A-29
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Best Local
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                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: Patentin Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/687,080 FILING DATE: U7-101-1996 CLASSIFICATION: 435 APPLICATION DATA: APPLICATION NUMBER: US/08/592,126 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 271.2; DB 2;
Pred. No. 4.9e-76;
0; Mismatches 98;
                 2: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                        4600-0111.30
                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              NAME: Sholtz, Charles K. REGISTRAINON NUMBER: 38,615
REGISTRAINON NUMBER: 4615
REFERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 77.3%;
Matches 385; Conservative (
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TYPE: nucleic acid
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CORRESPONDENCE ADDRESS
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                                                     Palo Alto
                                                                                           USA
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                   ADDRESSEE:
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TREATMENT AND DIAGNOSIS OF BREAST CANCER
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CTGCAAGGGTAGTACAAAAGGGAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTG 1003
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                                                                                                         362 CATGAAAAAAACTGAGAAGAGACTGTNCCCTACAATGCCACCGGAGCAGAACTGCCC 421
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                                           2 AGAGGGTACCAGCCCCAAGCCTTGACAACTTCCATAGGGTGTCAAGCCTGTGGGTGCACA
                                                                                      GAAGTCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Stewn G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 247
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/598,326 FILING DATE: 20-Jun-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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STATE: Washington
COUNTRY: USA
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US-09-598-326-29
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                                                                                                                                                                   421
                                                                                                                                                                                                                                    422 CAGGCCATGGAAGCACAGCTCTTATATCAATGTGACCTGGATGTTGAGACATGGAATCCN 481
                                                                                                                                                                                                                                                                                                                                                                                                       242 GAACACTGCCTAATGAAACTGTGAGAAGATGGCCACTGTCATCCAGACACCAGAATGATA 301
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                                                              1122 --TGTGAAAGCAGCAGGGATGGAGTCTGTACCCTACAAAACCGTAGTGGCAGAGCTGACC
                                      1064 GATCCACTGACAGCTTGCAGCAT-GTGCCTGAAAAATCCACAGACACTCAGTGCCAGCC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09062451
Patent No. 6444550
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/062,451
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 247.4; DB 4;
Pred. No. 3e-69;
0; Mismatches 177;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
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TYPE: nucleic acid
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Best Local Similarity 68.6
Matches 424; Conservative
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STATE: Washington
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STREET: 63
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Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GAACACTGCCTAATGAAACTGTGAGAAGATGGCCCACTGTCATCCAGACACCAGAATGAAA
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                                                                                                                                                                                                                   Length
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Pred. No. 3e-69;
0; Mismatches 177;
NAME: Potter, Jane E.R.

REGISTATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 210121.41901

TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                18.0%;
68.6%;
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Matches 424; Conservative
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Pred. No. 1.7e-65;
0; Mismatches 320;
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 IGCCCIGIGICCCAGIIAA------
                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                           17.48;
59.48;
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Best Local Similarity 59.4
Matches 572; Conservative
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(15233:
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                      TYPE: DNA
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   TGCACCCTGACAATGTGATAAAAAAGAAAAACCCATTTTCTGAGGGGAAATTCAAGCTGG
                         5234 TGCACCCTGATCATGTGGTAGAAAAGAAAAACCCATTTTCTGGGGAGGAATTCAAGCCGG
                                                                                                AATATCTCCTGGACATGTCAGAGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGG
                                                                                                                                                                      TGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAG
                                                                           CTGCAGAAATTTGCATATGTAATGAGGAGCTGAATG-TTAATCCTCAAGACAATGGGGAA
                                                                                                                                                                                                                            670 CCTAGGAGAAAATGGTTTTGTGGGACAGGCCCAGGGTCCCTGTGCTGTGTGCAGCCTAGA
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Pred. No. 7.9e-07
0; Mismatches 6
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APPLICANT: Bergilind Ran Olafsdottir
APPLICANT: Bergilind Ran Olafsdottir
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09426290 Patent No. 6410712
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Best Local Similarity 61.0%;
Matches 111; Conservative
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                   72077 GGAATCAA---AGATTATGTTGCAGCTTTAAGGCTTAATGTTTTCCCTGTCAATTTCAGG 72133
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 GAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGACCTGGACGTGAGACAT 1230
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Pred. No. 1.7e-54;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PROG APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTON ROPELSATO:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTONEY/AGENT INFORMATION:
WAND: CLASSIFICATION COMPATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TILLE OF INVENTION: Human RAD50 Gene and Met
; VORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sholtz, Charles K.
REGISTRATION UNDRER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 59:
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68.5%;
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LENGTH: 14855 base pairs
TYPE: nucleic acid
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Best Local Similarity 68.5
Matches 340; Conservative
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ORIGINAL SOURCE:
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72194 ACC 72196
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STATE: CA
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.4; DB 2;
Pred. No. 2.7e-05;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/463,91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.5%;
Best Local Similarity 48.8%;
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sing
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CITY: Lexington
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US-08-463-911-6
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63497 CTAAAAGCATGGGGACCCAGGCAGAGACTTGTCACAGGGACAGAGCCATGGCTGAGAGCC 63438
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                                                      826 GCAAAGAAGTCAAGAATTGAGGTTTGGGAA---CCTCCAATCAGATTTCAGAAGATATAT 882
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Best Local Similarity 4.9%; Pred. No. 5.7e-05;
Matches 17; Conservative 192; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30472/114 IMMU
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1800 Diagonal Road, Suite 500
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/ABENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)834109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149,
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1107;
                                                                                                                                                                                    APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.4; DB 3;
Pred. No. 0.0021;
0; Mismatches 101;
                                                                                                                                                                                                                                                       FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: WHI95-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
                   Sequence 217, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      794 CCTGGCCATCGGCCTAGTGCACAA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 GGTGAATATTTGGCTAATGAGGAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08463911
Patent No. 5869330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.1%;
Best Local Similarity 50.5%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                 APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hami
STREET: Two Mil:
CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02173
US-09-188-930-217
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rat
US-09-188-930-217
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1107
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US-08-463-911-1
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STATE:
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                                                                 341 GTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAGGAGAACCTGGAGAAGGTGCCT--- 397
                                                                                                                                                                                                                                                                                                   281 GAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATGTTGAGCTGCATC 340
                                                                                                                                                                                                                                                                                                                             235 ATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCGGGGGCTGAAG 294
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                                                                                                                 CTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAACTTCCTCTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION:
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.4; DB 4;
Pred. No. 5.8e-05;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                           575 TGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACA 610
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
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US-09-140-804-9
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2; Length 1276;
Pred. No. 0.013;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 ATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION NUMBER: BCT/US92/02469
PRIOR APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
TYPE: nucleic acid
STRANDENESS: single
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                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                          Query Match 2.9%;
Best Local Similarity 49.1%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                       ; LOCATION:
US-08-463-911-1
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1283 TTCGGACTTATATGGGGCCCGTACCCCTTTGTTTTGGCCAATTTTTCCATTTGGAACTG 1342
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                                                118-7704/PCT/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1343 CCGTATTTACCCAATGCCTGTACCTCCATTGTAT 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1624 TAATATCCATCCTATGTTTGTCCCACTATTGTAT 1657
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REFERENCE/DOCKET NUMBER: 118-7
TELECOMUNICATION INFORMATION:
TELEPHONE: 908-522-6955
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1755 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.8%
                                                                                                                                                                                                                                                                                                                                      mat_peptide
339..986
                                                                                                                                                                                                                                                                                                     339..986
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ANTI-SENSE: NC
FEATURE:
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FEATURE:
                                                                                                                                                                                                                                                                                    NAME/KEY:
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February 19, 2003, 15:08:07 ; Search time 476.571 Seconds (without alignments) 6506.903 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 2185239 seqs, 1125999159 residues
                                                                                                        US-09-997-610-1_COPY_2_1378
1377
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                               Title:
Perfect score:
Sequence:
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                                              OM nucleic
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human genset metab	Human cDNA sequenc	Human osteoblast d	Human genomic regi	Rhesus gene locus:	Rhesus dene locus:	Rhesus dene locus:	Rhesus gene locus:	Human DÑA represen
SUMMARIES	AAL44066	AAH14327	ABQ88125	ABN85735	AAS03687	AAS03689	AAS03690	AAS03688	ABK12169
DB	24	22	24	24	22	22	22	22	24
% Query Match Length DB	1338	2590	109201	155074	3093	9236	9236	9241	98690
% Query Match			46.8	46.5	46.5	46.5	46.5	46.5	45.8
Score	1281	663	643.8	640	639.8	639.8	639.8	639.8	631
Result No.	1	7	с С	O 4	c S	9	c 2	œ ن	o 0

617. 4 41.8 320.2 AAND03514 Human secreted by 160.2 8 41.8 030.2 AAND03514 Human secreted by 160.2 8 41.8 030.2 AAND03514 Human convolution of the		10	618.4 618.2 618.2		6063 465237 465237	222	AAL03635 ABQ87681 ABA90193		Human Human Human	reproductive oestrogen re oestrogen re	000
6012.8 44.8 0.002.2 AAA1303.4 Human CDPA S93.6 643.3 21250 22 AAS44505 Human CDPA S93.6 43.3 2127 22 AA56365 Human LERTI S93.6 42.8 21217 22 AA56365 Human LERTI MUMAN EXCIPED A 2.1 1465 22 AAS46365 Human Immune CDPA S53.8 40.9 8387 22 AA868324 Human DEPON CONCING S53.8 40.9 8387 22 AA868424 Human DEPON HUMAN DEPON CONCING S53.8 40.4 165 22 AA84722 Human DEPON HUMAN DEPON CONCING S53.8 40.4 165 22 AA87724 Human DEPON CONCING S53.8 40.4 165 22 AA87724 Human DEPON CONCING S53.8 80.9 1946 22 AA87724 Human CONCING S74.8 80.9 1946 22 AA87724 HUMAN CONCING S74.8 80.9 1940 1940 1940 1940 1940 1940 1940 194	٠	13	617.4		,	22	AAD05134			secreted pro	0
595.6 43.3 12509 22 AAS44505 Hunan LEKTI 590.8 42.9 1272 22 AA54505 Hunan LEKTI 590.8 42.9 1272 22 AA54505 Hunan ELKTI 590.8 42.9 1272 22 AA56505 Hunan ELKTI 590.8 42.9 1272 22 AA56505 Hunan ELKTI 590.4 42.8 1212 22 AA56950 Hunan immune 550.4 42.1 1465 22 AA59954 Hunan immune 550.8 40.9 837 22 AA59994 Hunan immune 550.8 40.9 837 22 AA59994 Hunan nervoul manus 550.8 40.9 837 22 AA59994 Hunan nervoul 550.8 40.9 837 22 AA59994 Hunan nervoul 550.8 40.4 1621 22 AA59994 Hunan nervoul 550.8 40.1 160.8 20.8 40.1 160.8 20.8 40.1 160.8 160		15	616.8		1736	222	AALU3634 AAH13678			reproductive	യധ
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99JP-0300253.
2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
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                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity; impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; and heart diseases (e.g. cardiac insulficiency, coronary insulficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present CDNA
                                                                                                                                                        or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     Treating or preventing a metabolic-related disease or disorder, e.g. obesity, impaired glucose tolerance, insulin resistance, Syndrome X, Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGCCTAGGAGAAAATGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1281; DB 24; Length 1338;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1338 BP; 359 A; 288 C; 350 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                             Tanaka
                                                                                                                                                                                                                                                                                                                                                                                sequence encodes the human GMG-9 protein.
                                                                                                                                                                                               Disclosure; Page 122-124; 128pp; English.
                                                             B,
                                                             Bihain
                                                                                                                                                                                                                                                                                                                                                                                                                                        93.0%;
ilarity 99.6%;
Conservative (
16-JAN-2001; 2001US-262235P
                                                             BA,
                                                                                       WPI; 2002-557821/59
                                                           Bour
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                       P-PSDB; AA015423
                             (GEST ) GENSET
                                                           Erickson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1284;
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                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602

[ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises a least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide which sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connected and on additional any specialised methods. AAH13628 and
AAH13613 to AAH13629 to AAH13632
ceptresent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

48.1%; Score 663; DB 22; Length 2590;
Best Local Similarity 80.7%; Pred. No. 7.5e-197;
Matches 826; Conservative 0; Mismatches 160; Indels 37.
                                                                        aito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2590 BP; 722 A; 526 C; 670 G; 672 T; 0 other;
                                                                           Saito
                                                                                                                                                                                                                      Claim 8; SEQ ID 11697; 2537pp + CD ROM; English.
                                                                                       Wakamatsu A, Nagai K,
                                                                        Hayashi K,
                                                                        Nishikawa
02-MAY-2000; 2000JP-0183767.09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                            (HELI-) HELIX RES INST.
                                                                                       Sugiyama T,
                                                                                                                   WPI; 2001-318749/34.
                                                                        Isogai T,
                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699
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                                                                                                GTACAAAAGGGAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATCT 1014
                                                                                                                                                                                                                                                                                                                AGTAGAGCTGTGAGAAGAAGTCCACCATCCTCCAGACTCCAGAAGGGTAGATCCACTGAC 1074
                                                                                                                                                                                                                                                                                                                                     AGCTTGCAGCATGTGCCTGAAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGCA 1134
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                                                                           894
                                                                                                                                                       954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell differentiation; bone tissue deposition;
                                                                                                                                                       ATGCCCAGGCAGAAGTTTGCTGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGTA
                                                                                                                                                                                                                                                       TACCTCTTGCATTGTCATGACCTGGACGTGAGACATGGAGTCAAAAGACATCATTTTGGA
                                                                           TCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human osteoblast differentiation related cDNA SEQ ID NO 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125/c
ABQ88125 standard; cDNA; 109201 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis; osteopathic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
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26-DEC-2001; 2001WO-US49808
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21-DEC-2001;
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                                                                                                                                                                                                                       can screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition;

(b) diagnosing abnormal deposition;

(c) treating abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporsis; or monitoring the progression of bone tissue deposition.

(c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

(c) treating or male osteoporosis, osteopenia, osteodystrophy, osteoporosis or male osteoporosis, osteopenia, osteodystrophy, osteoporosis or male osteoporosis, osteopenia, osteodystrophy, that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, fancon, syddrome or fibrous dysplasia. The present sequence is that of an osteoplast differentiation associated CDNA marker of the invention.

(c) specification, but was obtained in electronic format directly from WIPO
                                                                             Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22599 AAGCATTAAAGAGATGACTTGGGTGCTGTTAAAAGCATTTATTATTATAAGGGAAGCAG 22540
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                                                                                                                                                                                            The invention relates to genes and their expression profiles are used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTCAGTTTCATAAGGGAGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 643.8; DB 24; Length 109201;
Pred. No. 7.3e-190;
0; Mismatches 177; Indels 43; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109201 BP; 32871 A; 23488 C; 22108 G; 30734 T; 0 other;
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                                                                                                                                                            Claim 1; SEQ ID NO 32; 78pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
 Jaiswal N,
 Cook JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.8%;
Best Local Similarity 79.3%;
Matches 843; Conservative
                                                WPI; 2002-557663/59
 Axelrod DW,
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11824 GCAAAGCCACAGGGGTGAACTGAAGACTATGGGAACCTACTTGCATCAGGTGTG 21765
                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying modulators of taste signaling in taste cells for use in food and pharmaceutical industries to customize and regulate taste, by determining effect of the compound on a taste cell-specific ion channel
                                                                                                                                     GGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATCTAGTAGAGCTGTGAGAAGAA 1033
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                                                                                    AACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTG
                                                                    CTGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGGTAGTACAAAAGGGAAATGTTG
                                                                                                                                                         1094 AAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGCAGGGATGGAGTCTGTACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic region containing the ltrpc5 gene SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21644 TITGGAATGGCTGTATTACTCAATGCCTGCATCCCTATTGTA 21602
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2001US-0026188.
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The invention relates to identifying (MI) a compound that modulates taste signalling in taste cells, by contacting the compound with a eukaryotic constraint of the cell or cell membrane which expresses a taste cell-specific ion channel subunit (TC-ICS), and determining a functional effect of the compound upon a transmembrane ion flux of a predetermined ion, dentifying a compound that modulates taste signalling in taste cells.

(MI) is useful for identifying a compound that modulates taste signalling in taste cells, for identifying a compound that modulates taste signalling in taste cells, for identifying a compound that binds to a taste cell specific ion channel subunit and for modulating taste signalling in taste cells of a mammal, in particular a human. Modulators identified by (MI) care used by the food and pharmaceutical industries to customize taste.

CC e.g. as additives to food or medicine so that the food or medicine tastes of ifferent to the subject who ingests it. Bitter medicines can be made to caste less bitter and sweet substance can be enhanced. The modulators are useful for pharmacological and genetic modulation of taste signalling bathways. The taste modulators can be enhanced. The modulators are subjects for modulation of taste in vivo. The present sequence is that of the human genomic region (Chromosome Ilpis-5) containing the ltrpc5 gene
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Pred. No. 1.4e-188;
0; Mismatches 160;
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Best Local Similarity 80.6%;
Matches 825; Conservative (
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                                                                                                                   CTACCTCTTGCATTGTCATGACCTGGACGTGAGACATGGAGTCAAAAGAGATCATTTTGG 1253
                                                                                                                                                                 AGCTTTAAGATTTGACTGCCCCACTGGATTTCGGACTTATATGGGGCCCGGTA-CCCCTTT 1312
                                                                                                                                                                                                                GTTTTGGCCAATTTTTCCATTTGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for detection of common individuals, comprises RHD, SMP1
                                  Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
                                                                     1134 AGGGATGGAGTCTGTACCTACAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAAT
                       CAGCTTGCAGCATGTGCCTGAAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGC
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/note= "Binding site of primer rnb31"
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/note= "Binding site of
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D-negative
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The Rhesus genes and continuous the Rhesus genes and continuous comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus box(se), preferably the hybrid Rhesus box, the upstream Rhesus box and/or the downstream Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the common RHD negative haplotypes. In D-negative
containing whether a patient can be transfused with RhD negative blood and whether blood is suitable for transfusion to patients who should not be exposed to antigen C; (4) assessing the risk of a RhD negative mother of conceiving or carrying an RhD positive foetus. Anti-D antibodies are useful for treating pregnant women who are Rhesus D negative, where the foetus is not homozygous for the RHD gene to treat or prevent haemolytic disease of the newborn.
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                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                 DB 22; Length 3093;
                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.6e-189;
0; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                               Sequence 3093 BP; 891 A; 754 C; 619 G; 829 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Score 639.8;
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The sequence represents the coding sequence of Rhesus gene locus: upstream Rhesus box of D positives. The Rhesus genes locus comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or the downstream Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the RHD deletion in the common RHD negative haplotypes. The sequence has been used to design primers which are useful for: (1) the specific detection of the common RHD positive haplotypes in D-negative individuals; (2) blood group typing; (3) determining whether a patient can be transfused with RhD negative blood and whether blood is suitable for transfusion to patients who should not be exposed to antigan c; (4) assessing the risk of a RhD negative mether of conceiving or carrying an RhD positive foetus. Anti-D antibodies are useful for treating pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecular structure, useful for detection of common RHD positive haplotypes in D-negative individuals, comprises RHD, SMP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
AAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGCAGGGATGGAGTCTGTACCCT
                    ACAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATG
                                                                                         1214 ACCTGGACGTGAGACATGGAGTCAAAAGAGATCATTTTGGAGCTTTAAGATTTGACTGCC
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31-MAY-2000; 2000EP-0111696.
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                                                                                                      351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                                                                45; Gaps
  not homozygous
          haemolytic disease of the newborn
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                                                          Length 9236;
                                  Sequence 9236 BP; 2467 A; 2319 C; 2000 G; 2450 T; 0 other;
                                                        Score 639.8; DB 22; Length
Pred. No. 3e-189;
0; Mismatches 177; Indels
 where the foetus is
          the RHD gene to treat or prevent
who are Rhesus D negative,
                                                      Query Match 46.5%;
Best Local Similarity 79.1%;
Matches 841; Conservative 0
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The sequence represents the coding sequence of Rhesus gene locus:

downstream Rhesus box of D positives. The Rhesus genes locus

comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box

chromosome 1 p34.1-p36. Rhesus box. The RHD and RHCE genes are located at

chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the

RHD deletion in the common RHD negative haplotypes. The sequence has

been used to design primers which are useful for: (1) the specific

detection of the common RHD positive haplotypes in D-negative

individuals; (2) blood group typing; (3) determining whether a patient

can be transfused with RhD negative blood and whether blood is suitable

for transfusion to patients who should not be exposed to antigen C: (4)

ssessing the risk of a RhD negative mother of concelving or carrying an

RHD positive foetus. Anti-D antibodies are useful for treating pregnant

women who are Rhesus D negative, where the foetus is not homozygous for
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   CCACTGGATTTCGGACTTATATGGGGCCCGGTACCCCTTTGTTTTGGCCCAATTTTTTCCAT 1333
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                                     Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
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Pred. No. 3e-189;
0; Mismatches 177; Indels 45;
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                                                                                                                                                                     BADEN WUERTTEMBERG
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79.1%;
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31-MAY-2000; 2000EP-0111696.
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                                            GCATAAAAGTTCGGAAAATTTGCAGCCTGACAATGTGATAGAAAAGAAAATTCCCATTT
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AAS03688/c ID AAS03688 standard; DNA; 9241 XX

RESULT

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The sequence represents the coding sequence of Rhesus gene locus:
hybrid Rhesus box of RHD negatives. The Rhesus genes locus
comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the
RHD. SMP1 and RHCE (all undefined) genes and/or the
and/or the downstream Rhesus box. The RHD and RHCE genes are located at
chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 2 p34.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 2 p4.1-p36. Rhesus box flanks the breakpoint region of the
CHTOMOSOME 2 p4.1-p36. Rhesus box flanks the breakpoint and the sequence has
CHTOMOSOME 2 p4.1-p36. Rhesus box flanks have mother of conceiving or carrying an
CHTOMOSOME 2 p4.1-p36. Rhesus b negative mother of conceiving or carrying an
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for
CHTOMOSOME 2 p4.1-p36. Rhesus D negative, where the foetus is not homozygous for the RHD gene to treat or prevent haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                  SMP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid molecular structure, useful for detection of common positive haplotypes in D-negative individuals, comprises RHD, SMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTCAGTTTCATAAGGGAGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9241 BP; 2454 A; 2320 C; 2014 G; 2453 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                     Rhesus gene locus: hybrid Rhesus box of RHD negatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3e-189;
0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000; 2000WO-EP10745
                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1999; 99EP-0121686
31-MAY-2000; 2000EP-0111696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 79.1
Matches 841; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagner FF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid
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and RHCE genes
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                                                                                                                                                                                                                            Homo sapiens.
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replace (3319,G)
/tag= "
/tabel= SNP
/note= "Single-nucleotide polymorphism"
replace (3906,C)
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32173..82370
(*tag= i
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/label= SNP
/note= "Single-nucleotide polymorphism"
94400..94691
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/label= SNP
/note= "Single-nucleotide polymorphism"
1396..82172
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/label- SNP
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replace (94821,C)
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/note= "Single-nucleotide polymorphism"
replace (94892,T)
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/note= "Single-nucleotide
replace (94960,G)
   location/Qualifiers
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                                                                                                                                "TACR1"
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          replace (3164,G)
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/*tag= m
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90519..92675
/*tag= 1
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82371..90369
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90370..90518
/*tag= k
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4007..4395
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  Human; ds; gene; TACR1; Tachykinin receptor 1; chromosome 2;
SNP; single nucleotide polymorphism; gene therapy; haplotype; genotype;
pain; depression; vomiting; acute inflammatory diarrhoea;
oplate addiction; drug screening.
                                                           5455
                                                                                                                                                                                                                                                                                                                                          5814 AATTCCCAAGACAATGGGGAAAATGTCTCCAGGGCATGTCAGAGGTCTTTATGGCAACCC 5755
                                                                                                       5634 CTGACGGGAGGCAAGGTAGAGCTTGGGCTGTAGCTTCGGGGAGTGCAAGCCCCAAGCCTT 5575
                                                                                                                                        974 GGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATCTAGTAGAGCTGTGAGAAGAA 1033
                                                                                                                                                                                                                                                                        1034 GTCCACCATCCTCCAGACTCCAGAAGGGTAGATCCACTGACAGCTTGCAGCATGTGCCTG 1093
                                                                                                                                                                                                                                                                                  1094 AAAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGGAGGGATGGAGTCTGTACCCT 1153
                                                                                                                                                                                                                                                                                                                                                                                                               CCACTGGATTTCGGACTTATATGGGGCCCGTACCCCTTTGTTTTGGCCAATTTTTCCAT 1333
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                                                                                                                                                                                                    CTGTAGGGGTGGGGTCCTCATGGAGACCTCTGCAAGGGTAGTACAAAAGGGAAATGTTG 973
                          649 ATCAAATCACTGGCCTGGAGGCCT-AGGAGAAAATGGTTTTGTGGGACAGGCCCAGGGTC 707
                                                                                                                                                                           AACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTG
                                                                                              -------ATTCAGCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTT
                                                                                                                               GGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGG
                                                                                                                                                                                                                                                                                                                   Human DNA representing the Tachykinin Receptor 1, TACR1, gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTGTAT 1376
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ID ABK12169 standard; DNA; 98690
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The invention relates to an isolated polynucleotide sequence which comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of 16 SG as given in specification, where each SG comprises specific regions of the TACRI genomic DNA appearating as ABK12169, and is defined by 26 years and a percentage as ABK12169, and is defined by 4601, 94831, 94892, 94960. Also included are fragments of the morphisms at positions (P) 3164, 3119, 3906, 4339, 4444, 92915, 94601, 94831, 94892, 94960. Also included are fragments of the morphisms at positions (P) 3164, 3119, 3906, 4339, 4444, 92915, 24601, 94831, 94892, 94960. Also included are fragments of the morphisms at computed by determining either the haplotype of one or both copies of the TACRI gene, predicting the haplotype pair for the TACRI gene of an individual by determining either the haplotype of one or both copies of the TACRI gene, predicting the haplotype pair for the isolated oligonuclectide for detecting the copies of the TACRI gene, predicting the haplotype pair for the isolated oligonuclectide for detecting the polymorphisms, a computer system for storing and analysing polymorphism of protein for use in screening for TACRI and expressing TACRI and fugus and function of TACRI and expressing morphisms and baplotype data is useful for taldating whether TACRI is a suitable target for drugs to treat pair. The allocating whether an clindal has one of the haplotype pairs. The haplotype data is useful for secenting for treating a specific condition or disease predicted to be associated with TACRI activity. The method is also useful for validating a compounds to treat a specific condition or disease predicted to be associated with TACRI activity. The methods are useful for identifying an associated with TACRI activity. The method is also useful for TACRI activity or a disease, staging of a disease, or tresponse to a drug. The pene for TACRI is located on human character and every propertion or disease predicted to be a true. The pene for TACRI is located on huma
                                                                                                                                                                                                                                                                                                                                                Novel isolated polynucleotide which is a polymorphic variant of tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein isoform used in screening drug candidates to treat pain, depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 89pp; English.
                                                                                                                                                                          GENA-) GENAISSANCE PHARM INC
                                                                                                                         25-AUG-2000; 2000US-227815P.
                                                                        27-AUG-2001; 2001WO-US26663
                                                                                                                                                                                                                              Anastasio AE, Kazemi A;
                                                                                                                                                                                                                                                                          WPI; 2002-280907/32.
                                                                                                                                                                                                                                                                                                    P-PSDB; AAU78238
                       28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                              vomiting
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Human reproductive system related antigen DNA SEQ ID NO: 6323.
                                                                      AAL03635 standard; DNA; 6063 BP.
                                                                                                                      (first entry)
                                                                                                                                                                                  cancer; gene therapy; ds.
            50892 rgr 50890
                                                                                                                      21-NOV-2001
                                                                                               AAL03635;
            g
                                                                                              5.
                                                                                                                                           451 AGTTTCATAAGGGAGGCAGAGCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATA 510
                                               391 GAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTC 450
                                                                                                         43;
  Length 98690;
 Score 631; DB 24;
Pred. No. 7.1e-186;
                       0; Mismatches 160;
45.8%;
80.2%;
                          Conservative
            Similarity
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Sequence 98690 BP; 29293 A; 20385 C; 20052 G; 28885 T; 75 other;

4atches 820;

51846

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Query Match Local

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Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                51546 CCAGCCACTCCAGCTGTGGCTGAAAGGGGCCAATGTACAGCTTGGGCTGTGACTTCAGAG 51487
                                                                                                 GGTGCAAGCCCCAAGCCTTGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAG
                                                                                                                                                                                                                                                                              51486 GATGCAAGCCCCAAGCCTTGGCAGCTTCCACATGGTGTTGAGCCTGCAGGGTGCACAGAAG
                                                                                                                                                                                                                                                                                                                                          ATGCCCAGGCAGAAGTTTGCTGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGTA
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                                                                              TGTGGGACAGGCCCAGGGTCCCTGTGCTGTGTGCAGCCTAGAGACTTGGTGCCCTGTGTC
                                                                                                                                                            ---CTTCAGAG
                                                                                                                                                                                                                                                                                                                   TCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACAAAAGGGAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1075 AGCTTGCAGCATGTGCCT-GAAAAATCCACAGACACTCCAGGCTGCCAGCCTGTGAAAGCAGC
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AGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGCC---TAGGAGAAAATGGTTT
                                                                                                                                                            CCAGTTAATTCAGCTGTGG-----
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04-FEB-2000;
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TTTTGGCCAATTTTTCCATTTGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTG 1373
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                                        GGGATGGAGTCTGTACCCTACAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATC
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                                                                                                            Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                 Disclosure; SEQ ID NO 6323; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 6063;
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                                                                                                                                                                                                                                                                                                                     Sequence 6063 BP; 1655 A; 1162 C; 1259 G; 1987 T; 0 other;
                                      Ruben SM;
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.9%;
Matches 818; Conservative
                                                                                                          nucleic acid
                                    Barash SC,
                                                                       WPI; 2001-465570/50
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/standard_name= "Single nucleotide polymorphism" 243087306167 /*tag= b / number= 9 /*tag= 0	/*tag-a /*tadard_name="Single nucleotide polymorphism" replace(306382,G) /*tag-a /*tag-a 306504373639 /*tag-b /*umber=10 37364037378 /*tag-b /*umber=11 /*tag-b /*tag-b /*tag-b /*tag-b /*tag-b /*tag-b /*tag-b /*tag-b	/ number 11 422964423097 422964423097 / rag = b /*tag = a /*tag = a 423098456353 /*tag = b /*tag = b		I . I . I . I . I . I . I . I . I . I .	/*tag= a /*tag= as /*tag=
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GCTTTAAGATTTGACTGCCCCACTGGATTTCGGACTTATATGGGGCCCCGT-ACCCCTTTG

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                                                                                                                                                                                                                            Db 438730 CTGCTGTAGAGATTTGTGGAATTTGAACTTGAGAAATGATTTGGGGGTACCTGGTAAAA 438789
                                                                                                                                                                                                                                                                                                   Db 438790 GAAATTTCTAAGCAGCAAAACATTCAAAAGGTGACTTGGGTGTTGTTAAAAGCATTCTGT 438849
                                                                                                                                                                                                                                                                                                                                                        438968 CAAGGAGCCAAATGTTAATCCCCAAGACAATGGGGAAAATGTCTCCAGAGCATGTCATAG 439027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 439088 GTGGGCCAGTCCCAGGGTCCCCATGCTGTGCAGCCTAGGAACTTGGTGCCCTGCATCT 439147
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                                /standard_name= "Single nucleotide polymorphism" replace(460564,A)
                                                                                                                                                            43;
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                                                                                                                      Score 618.2; DB 24;
Pred. No. 1.9e-181;
0; Mismatches 193;
replace(460553,C)
/*tag= a
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larity 78.2%;
Conservative
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The present invention describes an isolated peptide (I) consisting of an amino acid sequence selected from: (a) the amino acid sequence of a variant of the oestrogen receptor alpha (EST-alpha) protein in AAG68251; (c) the oestrogen receptor alpha (EST-alpha) protein in AAG68251; (d) a fragment comprising at least 10 contiguous amino acids of the protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and vascince contaction. (I) is useful for identifying an agent that blinds to (I), by contacting (I) with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the peptide. A polynucleotide (II), encoding (I), is useful in the development of diagnostics and therapies for diseases and disorders mediated/modulated by an oestrogen receptor (ER). (II) is also useful in gene therapy for tracating cancer, osteoporosis and cardiovascular giseases. The human ESR-alpha gene is located on chromosome 6. The present sequence represents the human ESR-alpha gene, which is given in the exemplification of the present invention.
                                                                       Novel variant of estrogen receptor alpha polypeptide useful for determining the biological activity of a protein for high throughput screening and for raising antibodies that elicit an immune response in
                                                                                                                                                                                                                                                                                                                                                                                             Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2; synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic; cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis; cardiovascular disease; oestrogen receptor; ds.
TTTTGGCCAATTTTTTCCATTTGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTG
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                                                                                                                                                                                                                                                                                                                                                               Human oestrogen receptor alpha gene.
                                                                                                                                                                                                                                                      ABA90193 standard; DNA; 465237 BP
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24-JAN-2001; 2001US-0768184
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P-PSDB; AAG68251.
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Sequence 465237 BP; 133988 A; 89578 C; 93946 G; 147721 T; 4 other;
                                                                                                                                                      GAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAAGGCATTCAGT
                                                                                                                                            TTCATAAGGGAGGCAGAGCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATAAAA
                                                                                                                                                                                   AAGAAAAACCCA-TTTTCTGAGGGGAAATTCAAGCTGGCTGCAGAAATTTGCATATGTAA
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                                        Indels
                     DB 24;
                                       0; Mismatches 193;
                    Score 618.2; DB 24
Pred. No. 1.9e-181;
                                                                                                                                                                                                                                                                                                                                                   CAGTTAATTCAGCTGT------
                   Ouery Match
Best Local Similarity 78.2%;
Matches 847; Conservative
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AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted protein genes, and AAE01312-AAE0131 represent the proteins they encode. AAE01312-AAE01340 represent human secreted protein variants or fragments. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein-encoding gene 14 cDNA clone HISBF60, SEQ ID NO:24.
                            foctal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDAelmers's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
TTTTGGCCCAATTTTTCCATTTGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; proliferative disorder; cancer; tumour;
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/product= "Human mature secreted protein"
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216..353
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                                                                                                                      1374 TAT 1376
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2256 TTGGAGCCCCCACACAGAATCCCTACTGGGGCACCACTAGTGGAGGCGTGTGCGAAGAAGG 2315

CCACCATCCTCCAGACTCCAGAAGGGTAGATCCACTGACAGCTTGCAGCATGTGCCTGAA 

2316 1096

1036

δ QQ δ g ŏ QQ δ g ŏ g Qγ

AAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAG-CAGGGATGGAGTCTGTACCTA 1154

1155 CAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGA

CCTGGACGTGAGACATGGAGTCAAAAGAGATCATTTTGGAGCTTTAAGATTTGACTGCCC 2496 CCTGGATGTGAGACATGGAGTCAGAGGAGATCATTTTGGAACGNTATAATTTGACTGCCT

1215

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ALDS, autoimmune diseases (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma.

Parkinson's disease, cognitive disorders, schizophrenia, asthma.

Strin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in allegnostic immunoassays e.g., radioimmunoassay or enzyme linked in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
24 genes, based on the tissues in which they are most highly expressed, and include developing products for the disquosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1599 GAACTTTGATCTTGAGAGAGATGATTTAGGGTATCTGGCTGAAGAAATTTCTAAGCAGCA 1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 617.4; DB 22; Length 3203; Pred. No. 1.7e-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3203 BP; 868 A; 650 C; 740 G; 943 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 192;
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78.2%;
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2556 CGCTGGATTTTGGACTTGCATGGGGCTTGTAACGCCTTTGTTGTGGGCAGTTTCTCCCAT 2615

AAL03634 standard; DNA; 6063

RESULT 14 AAL0363 AAL03634;

CACTGGATTTCGGACTTATATGGGGCCCCGT-ACCCCTTTGTTTTGGCCCAATTTTTCCAT

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system related antigen; reproductive system disorder;
                                                Human reproductive system related antigen DNA SEQ ID NO: 6322.
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2000US-0214886.
2000US-0215135.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0198123.
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2000US-0184664
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                        (first entry)
                                                                                   gene therapy; ds
                                                                        reproductive
                                                                                                                                 WO200155320-A2.
                                                                                                           Homo sapiens.
                                                                                                                                                                                 17-JAN-2001;
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17-MAR-2000;
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07-JUL-2000;
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14-AUG-2000;
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                        21-NOV-2001
                                                                                                                                                         02-AUG-2001
                                                                                    cancer;
1837 TCTCCAAGACAATGGGGAAAATGTCTCCAGGGCATGTCACAGGTCTTCATGGCAGCCCCT 1896
                                                                                                                                                                                                        2076
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RR 14-AUG-20000 2000US-0225477
RR 14-AUG-20000 2000US-0225477
RR 14-AUG-20000 2000US-0225477
RR 14-AUG-20000 2000US-0225759
RR 22-AUG-20000 2000US-0225759
RR 22-AUG-20000 2000US-0225759
RR 22-AUG-20000 2000US-0225759
RR 22-AUG-20000 2000US-0225759
RR 10-SEP-2000 2000US-022576
RR 10-SEP-2000 2000US-022944
RR 10-SEP-2000 2000US-023944
RR 10-SEP-2000 2000US-023144
RR 10-SEP-2000 2000US-023144
RR 11-SEP-2000 2000US-02314
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 616.8; DB 22; Length
Pred. No. 3.9e-182;
0; Mismatches 192; Indels
                                                                                                           2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249208.
2000US-0249209.
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2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249217.
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2000US-0250160.
2000US-0250391.
2000US-0251030.
2000US-0251988.
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20000S-0251479.
20000S-0251856.
20000S-0251868.
2000US-0251869.
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2000US-0249212.
2000US-0249213.
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2000US-0249265.
2000US-0249297.
2000US-0249299.
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78.2%;
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Matches 832; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465570/50
                 08-NOV-22000

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08-NOV-2000

17-NOV-2000

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17-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
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3559 GCATAAAATTTGGAAAATTTGCAGCCAGTTGATGCAGCAGAAGAGAAACCTGTTTTT 3618
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                      4278 TGAAGCCACAGGGGCAGAGCTGCCCAAGACTAAGGGAACCTCTCTTGCATCATGTGA
                                            TCCTCAAGACAATGGGGAAAATATCTCCTGGACATGTCAGAGGTCTTCACAGCAGTCCAT
                                                                         CAAATCACTGGCCTGGAGGCCTAGGAG---AAAATGGTTTTGTGGGACAGGCCCAGGGTC
                                                                                                     CCTGTGCTGTGTGCAGCCTAGAGACTTGGTGCCCTGTGTCCCAGTTAATTCAG-----
                                                                                                                                  CAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGGAA
                                                                                                                                                                                            CCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTGCT
                                                                                                                                                                                                                         GTAGGGGTGCGTCCTCATGGAGAACCTCTGCAAGGGTAGTACAAAAGGGAAATGTTGGG
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                                                                                                                                                                                                                                                                                  CCACCATCCTCCAGACTCCAGAAGGGTAGATCCACTGACAGCTTGCAGCATGTGCCTGAA
                                                                                                                                                                                                                                                                                                                                            CAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGA
                                                                                                                                                                                                                                                                                                                                                                                                     CACTGGATTTCGGACTTATATGGGGCCCGT-ACCCCTTTGTTTTGGCCAATTTTTCCAT
              TGAGGGGAAATTCAAGCTGCCTGCAGAAATTTGCATATGTAATGAGGAGCTGAATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                 1334 TIGGAACTGCCGTATTTACCCAATGCCTGTACCTCCATTGTATG 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:10539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 1736
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence of the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the full-length
cDNAs easily without any specialised methods. AAH03658 and
AAH13633 to AAH13642 represent human amino acid sequences; and AAH13629 to AAH13632
crepresent clinear in the exemplification
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Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 GACAAGAAAAACCCATTTTCTGGGGAGAGAGTTCAAGCCAGCTGGGGAAATTTGTGTGAAGT 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 AGTTTCATAAGGGAGGCAGAGACATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATA
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Otsuki T;
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                                     GGGACAGGCCCAGGGTCCCTGTGCTGTGCAGCCTAGAGACTTGGTGCCCTGTGTCCCA
            AGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGCCTAGGAGAAAATGGTTTTGT
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Query Match Length

93.0 145880 50.5 193092 50.2 124518

1281 695.2 691 690.8 690.2 689

AC017063 Homo sapi AL138962 Human DNA AL353634 Homo sapi 269722 Human DNA s

Human DNA s 99 Homo sapi 77 Homo sapi

Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi

AC123595 AC026107 AC044889

HSU212C1 AC008799 AC025577 AC123595 AC026107 AC0914889 AC091005 AC010312

186660

174874

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40714 154090 67984 168502

131215 152544

681.6 680 679.8 679.8 679

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684.2

Homo sapi Human chr Homo sapi Human chr

AC010312 H AC091005 H AC079614 H AC012038 H AL359232 H AC01882 H AC0793588 H AC079899 H

CNS05TEJ AC011882

9614

AC093588 AC079899

146743 166679

176426

678.8 678.8 678.8 678.6

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February 19, 2003, 23:16:26 ; Search time 4390.26 Seconds (without alignments) 9128.055 Million cell updates/sec
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2003
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ALIGNMENTS

Human DNA sequence from clone RPI-302D9 on chromosome 22 Contains GSSs, complete sequence. 282198 on chromosome 22 Contains 282198. G:6572207 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (Dases 1 to 145880) Bridgeman, A. Direct Submission Homo sapiens. Homo sapiens RESULT 1 HS302D9 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE is the number of results predicted by chance to have a

. 9

Pred.

COMMENT

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// Note="Milb repeat: matches 1. .99 of consensus" 15490. .1562 / Note="Alusq1 repeat: matches 2. .114 of consensus" 15699. .15727 / Note="Milb repeat: matches 119. .178 of consensus" 15728. .16027
                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2553. .2706 of consensus" 8914. .9030 / note="MIR repeat: matches 147. .262 of consensus" 9110. .3280 / note="MIR repeat: matches 91. .262 of consensus"
                                                                                                                     /note="MADEL repeat: matches 23. 77 of consensus" 7482. 7754 /note="AluJb repeat: matches 9. 290 of consensus" 7775. 8060 /note="AluJo repeat: matches 1. 295 of consensus" 8414. 8551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2275 of consensus'
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/note="MIR repeat: matches 141. .225 of consensus"
14589. .14679
                                                                               .302 of consensus"
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15071. .15188
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                                                                                                                                                                                                                                                                                                                                                                             9283. '9412
/note="MIR repeat: matches 15. .144 of consensus"
9521. '9679
/note="FAM repeat: matches 3. .161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .425 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .150 of consensus"
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/note="MIR repeat: matches 63. .24

13017. .13369

/note="match: STS: Em:G49301"

13331. .13397

/note="MIR repeat: matches 174. .2

13398. .13698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Milksp repeat: matches 1...:
13699. .13810
/note="Milk repeat: matches 76..1'
13806. .13919
/note="Milk repeat: matches 77..18'
13945. .14060
/note="Milk repeat: matches 24..1'
14061. .14367
/note="Ally repeat: matches 1...'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 173.
14597. .15201
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5304. .15399
                                 note="MADE1 repeat: matches 1.
                                                                               note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ370601"
14868. .15040
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Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variationss together with a note of the overlapping clone name. Note that the variation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RP1-302D9 The true left end of clone CTA-282F2 is at 69682 in this sequence. The true right end of clone CTA-415G2 is at 55167 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22 RPI-302Dg is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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'note="MLTIE repeat: matches 136. .359 of consensus'
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1350. .2660
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188. .245
/note="MER3 repeat: matches 144. .209 of consensus"
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'note="MER5A repeat: matches 26. .187 of consensus"
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/note="AluSx repeat: matches 1. .312 of consensus"
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Moote="AluSp repeat: matches 1. .299 of consensus"
1450. .1583
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/note="AluSq repeat: matches 2. .300 of consensus"
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'note="THE1B repeat: matches 3. .364 of consensus"
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/note="MER3 repeat: matches 1.
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    .145880
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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'note="MLT1E repeat:
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/clone="RP1-302D9"
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20682. .21008
/note="AluSg1 repeat: matches 1. .306 of consensus"
21239. .21553
/note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
21882. .2254
                                                                                                                                                                                                                                             consensus,
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18393. 18712
18793. 18713
18713. 19133
/note="MER66-internal repeat: matches 4548.
                                            /note="Alux repeat: matches 1. .300 of conse 1825. .18323
/note="MSTA repeat: matches 2. .29 of consen 18324. .18392
/note="MER66-internal repeat: matches 4919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus"
23905. 23989
/note="MEK66-internal repeat: matches 3017.
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'note="HERVFH21 repeat: matches
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/note="AluSp repeat: matches 1.
/note="Alusc repeat: matches 1.
16028. .16245
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19231. 19719
/note="match: GSS: Em:B14179"
19537. .20290
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/note="33_copies 2 mer
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/note="MER66-internal
                      /note="MLT1B repeat:
16546. .16854
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ACAGAGTCCCCAGTGGGGCTCCATCTAGTAGAGCTGTGAGAAGAAGTCCACCATCCTCCA
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AUTHORS TITLE

JOURNAL

REFERENCE

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/rpt_family="MIR"
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/rpt_family="MER1_type"
6479 .6507
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6691 .6989
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9245. .9274
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/rpt_family="MIR"
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13297. 14044
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14366. 14429
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14565. 15340
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/rpt_family="AT_rich"
1737. .17522
/rpt_family="Alu"
17581. .17975
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/rpt_family="(TG)n"
12999. 13157
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3891..3996
/rpt_family="MIR"
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211. .1478
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479. .1490
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2394. .2715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-756P10, 2000 bp overlap; the clone sequenced to the right is RP11-818C3. Actual start of this clone is at base position 178381 of RP11-756P10; actual end is at base position 193092 of RP11-354H17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MG. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51.1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                        2 (bases 1 to 193092)
Boarright, E., Haakenson, W. and Doebber, A.
The sequence of Homo sapiens BAC clone RP11-354H17
Upublished (2001)
3 (bases 1 to 193092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web Site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0354H17
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1 (bases 1 to 193092)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                    4 (bases 1 to 193092)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 193092)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                       Waterston, R.H.
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Waterston, R.

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

AUTHORS TITLE

JOURNAL

REFERENCE

repeat\_region

There is an unresolved tandem repeat from 23045 to 24207

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bp DNA linear PRI 28-JAN-2001
P RPI1-279N8 on chromosome 13, complete
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Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (28-JAN-2001) Sanger Centre, Hinxton, Calone
Interpolated Sanger Centre
On Jan 29, 2001 this sequence version replaced gi:12584354.
On Jan 29, 2001 this sequence version replaced gi:12584354.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                 711 GIGCTGTGCAGCCTAGAGACTTGGTGCCCTGTGTCCCAGTTAATTCA------759
113577 GIGCTGTGTGCAGTCTAGGTACTTGGTGCCTGCATCCAGCCACTCCAGACATGACTAA 113518
                                                                                                                                                                  Db 112977 TGGATTTTGGACTTGCACGGGGCTTGTAACCCCTTTGTGGGCCAATGTCTCTCATTG 112918
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Catarrhini; Hominidae; Homo.
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                                                                                    -----GCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTTGGCA
                                                                                                                                                   GCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGGAACC
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Human DNA sequence from clone
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Bates, K.
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AL138962
AL138962.16
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Pred. No. 5.8e-195;
0; Mismatches 173;
                         /rpt_family="L1"
20140. 20312
/rpt_family="MER1_type?"
20468. 21181
/rpt_family="L2"
21208. 21485
                                                                                                             21<u>208</u>. .21485
/rpt_family="MER1_type"
21488. .21697
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23351. 23528
/rpt_family="(CAGA)n"
23595. 23832
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23822. 24006
/rpC_family="(CA)n"
24018. 24148
/rpt_family="(CA)n"
25078. 25559
/rpt_family="1"
27832. 27895
/rpt_family="1"
27832. 27995
/rpt_family="1"
27967. 27995
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30597. .30777
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28974. . . 2026.1
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22636. .22815
                                                                                                                                                                                                                                                               /rpt_family="(CA)n"
22877. .23053
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23075. .23388
                                                                                                                                                                                              /rpt_family="ERVL"
22519. .22567
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29271. .29301
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30833. .30908
                                                                                                                                                      /rpt_family="L2"
22183. .22404
/rpt_family="L1"
18061. .18371
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Best Local Similarity 80.5
Matches 853; Conservative
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AL353634 77405 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome X clone RP11-435A2 map q21.33-22.3, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66296 GGGTGCAAGCCCTAAGCCTTGGCAGCTTCCACATGTTAAGCCTGTGAGTGCACAGAA 66237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: Jassmid. 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 13% of reads Chemistry:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65936 TGGGAGGGAGACTGTACCATGCAAGACCACGGGCAGAGCTGCCCAAGACCATGGGAAC
                                                                         66236 ATCAAGAACTGGGGTTTGGGAACCTCTGTCTAGATTTCAGAGGATATATGGTAATACCTG
                                                                                                                                                               AGTACAAAAGGCAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATC
                                                                                                                                                                                                                                                      1014 TAGTAGAGCTGTGAGAAGAAGTCCACCATCCTCCAGACTCCAGGAAGGGTAGATCCACTGA
                                                                                                                                                                                                                                                                                                                                             1074 CAGCTTGCAGCATGTGCCTGAAAAATCCACAGACACTCCAGTGCCAGCCTGTGAAAGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1314 TITIGGCCAATTITITCCATTIGGAACTGCCGTATTTACCCAATGCCTGTACCTCATTG
                                                      GTCAAGAATTGAGGTTTGGGAACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTG
                                                                                                                                           GATGCCCAGGCAGAAGTTTGCTGTAGGGGTGGGGGTCCTCATGGAGAACCTCTGCAAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
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HTG; HTGS_PHASE2; HTGS_CANCELLED.
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORNPEP; Information http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-279NB it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-279NB is at 12451B in this sequence. The true left end of clone RP11-52BD24 is at 114969 in this sequence. The true right end of clone RP11-214011 is at 100 in this sequence.
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                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr13
RP11-279N8 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66597
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                                                                                                                                                                                                                                                                                                                    Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 691; DB 9; Length 124:
Pred. No. 9.9e-194;
0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                 of Pieter de Jong. For further detail
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
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/clone_lib="RPCI-11.1"
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AUTHORS
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KEYWORDS
SOURCE
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HSU212C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 AAGAAAAACCCA-TTTTCTGAGGGGAAATTCAAGCTGGCTGCAGAATTTGCATATGTAA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             573 TGAGGAGCTGAATGTTAATCCTCAAGACAATGGGGGAAAATATCTCCTGGACATGTCAGAG 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGGCAGAAGTTTGCTGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGTAGTA 957
                                                                                                                                                                                                                                                                                                                                                                                                   CTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAA 393
                                                                                                                                                                                                                                                                                                                                                                           Gaps
Dye-terminator Big Dye; 86% of reads
Consensus quality: 76604 bases at least Q40
Consensus quality: 77098 bases at least Q30
Consensus quality: 77320 bases at least Q20
Insert size: 77405; sum-of-contigs
Insert size: 85298; 1:% error; agarose-fp
Quality coverage: 4.54 x in Q20 bases; sum-of-contigs Quality
coverage: 4.30 x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAGCCCCAAGCCTTGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCA
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                                                                                                                  * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                               Length 77405;
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                                                                                                                                                                                                                                                                                                                                               Score 690.8; DB 2;
Pred. No. 1.1e-193;
0; Mismatches 172;
                                                                                                                                                                                                                                                   /clone="RP11-435A2"
/clone_lib="RPCI-11.2"
1. 77405
1. 77405
14551 c 15133 g 22649 t
                                                                                                                                                                                    1. 77405
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                        /map="q21.33-22.3"
                                                                                                                                                                                                                             /chromosome-"X"
                                                                                                                                                                                                                                                                                                                                                50.2%;
80.6%;
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Best Local Similarity 80.6
Matches 871; Conservative
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Direct Submission
Submitted (22-FEB-1995) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (22-FEB-1995) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk
IMPORTANT: This sequence is the entire insert of clone U212C1. The
true left end of clone U212C1 is at 1 in this sequence. The true
right end of clone U212C1 is at 40714.
U212C1 is from the human chromosome X-specific cosmid library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSU212C1 40714 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from cosmid U212C1, between markers DXS366 and DXS87 on chromosome X.
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Homo.
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ATGGAGTCTGTACCCTACAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTAC
                                                                                                                                                                                                                                                                                       TTGCAGCATGTGCCTGAAAAATCCACACACACTCAGTGCCAGCCTGTGAAAGCAGCAGGG
                                                                                                                                                                                                                                                                                                                                                      CTCTTGCATTGTCATGACCTGGACGTGAGACATGGAGTCAAAAGAGATCATTTTGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="13 copies of 2 mer 100 % conserved"
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7.0cte="Lil element fragment"
2571. 2617
7.0cte="MER43 element fragment"
2613. 5203
7.0cte="Lil element fragment"
5204. 5229
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/note="MER43 element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 element fragment"
388. 758
/note="L1 element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="LLOXNC01-212C1"
/clone_lib="LLOXNC01"
10..233
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Odell, C.
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4;

Gaps

513

572

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24783 TGCACCGTGGACAAAAACCGGCAGACACTCAATGCCAGCCTGTGAAAGCAGCAGGGA 24842
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                                                                                                                                                                                                                                                                                                                                            334 CIGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAA 393
                            consensus,
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                                                                                    consensus,
                                                                                                                                                                                                                                                                    Length 40714;
                                                                            /note="Alu repeat: matches 93. .1 of consens 3223. .32735
/note="MER9 element fragment"
35.168. .35.654
/note="MER4B element fragment"
40.640. .40.693
/note="27 copies of 2 mer 94 % conserved"
1 a 7879 c 8141 g 13150 t
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                            .109
                                                                                                                                                                                                                                                                      50.1%; Score 690.2; DB 9; 80.6%; Pred. No. 1.5e-193;
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31981. 32073
7.partial
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870; Conserv
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/note="MuT1A element fragment"
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30032. 30159
/note="WRR5 element fragment"
31794. 31980
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28319. .28608
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16204. .16495
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Db 108157 CTTGTGCTGTGTGCAGCTTAGGGACTTGGTGCCCTGCATCCCAGCTGCCATGGC 108216
Db 108337 ACCTCCACCTAGATTGCAGATGATGTATGGAAATGCCCGGGTGACCAGGAGAAGTTTGC 108396
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Homo sapiens chromosome 5 clone CTD-2061E19, complete sequence.
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Submitted (28-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 28, 2002 this sequence version replaced gi:19224702.
Draft Sequence Produced by DOE Joint Genome Institute
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Creek, CA
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DOE Joint Genome Institute and Stanford Human Genome Cen
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute.

Direct Submission

Genome Institute, 2800 Mitchell Drive, Walnut (3 (bases 1 to 123098)

Direct Submission
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Quality: Phrap Quality >-40 99.8% of Sequence;
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Alebrooks S.L. Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. (Dassas I to 154094)

Alebrooks S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Alebrooks, S.L., Amaratunge, H.C., Are, J.R., Bonnin, D., Bouck, J., Bundock, S. Brieva, M. Blankenburg, K., Bonnin, D., Bouck, J., Buhay, C., Burchon, T.F., Bentcon, J. Blankenburg, K., Bonnin, D., Bouck, J., Chack, J., Chack, J., Chack, J., Carelland, C.D., Correr, J. Butch, D. Ghowdhry, I., Christopoulos, C., Clereland, C.D., Cox, C., Coyle, M.D., Datborne, S.R., Davila, R.L., Dapacr, H., Doughanit, J., Branchart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Perraguco, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Perraguco, D., Carcial, J., Chack, J., Draper, H., Dugan Rochas, S., Durbin, M.H., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Perraguco, D., Garcial, A., Gao, J., Carcial, A., Gao, J., Carcial, A., Garcial, A., Gao, J., Rango, M., Holle, S., Hamilton, R., Han, J., Herrandez, O., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hollson, M., Havlak, P., Hawes, M., Hall, W., J., Harris, C., Harris, C., Harris, C., Harris, C., Hollson, B., Howard, S., Huber, J., Hulk, S., Hume, J., Harris, C., Harris, C., Hollson, D., Hodgson, B., Hall, M., Han, D., King, L., Korvah, J., Kovar, C., Lavis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Lui, A., Martindale, A., Martindale, A., Martindale, A., Martindale, A., Martindale, M., Marbins, P., Marchin, Mapha, P., Marchin, Mapha, P., Marchin, Mapha, M., Marchin, M., Mapha, M., Marchin, M., Mapha, M., Marchin, M., Mapha, M., Marchin, M., Sison, I., Shan, Y., Hamerisa, A., Tamerisa, M., Stone, H., Stone, H., Stone, M., Socti
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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC025577.15 GI:9910028
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

## ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:511-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

## QUALSTAT-REPORT-------

154090 153545 0.000261755 22 0	Edited-Conte attraccett cutraccett cutraccacag(t) cutractatt(t) ttractatt(t) ttractatt(t) acaacacaag(a) caacacaag(a) caacacaag(a) caacacaag(a) caacacaag(a) caacacaag(a) tractatty(t) tractatty(t) acaacacaag(a) caacacaag(a)	a (t)
gth: es in estimate: ror rate (BCM-Phrap estimate) f Phrap values less than 40 : consensus changing edits: N's in consensus :	Original+Context acacagacc(n)tttttttt atttgccct(n)tagaaaaga ctgtcaccag(n)aaaagatcca agcaatgcag(n)gagaaaga ctttactatt(n)tgtttattcta tttactattn(f)tttattcta ttactattn(g)tttattcta acaacaag(n)tagtttgg caacacaag(n)tagtttgg caacacaag(n)tagtttgg caacacaag(n)tagtttgg ntagtttgg(n)ttactcttcc cattgaccc(n)ctgtcattc actgcacct(n)tgcctcccca actgcacct(n)tagtcattc actgcacct(n)tagtcattc actgcacct(n)tagtcatcc actgcacct(n)tagtcatcc actgcacct(n)tagtcatcc actgcacct(n)tagtcatcc actgcacct(n)tagtcatcc actgcacct(n)tagtcatcc	cctagaaaaa(n)gacntttct ttctttttta(n)ttttctttt tantttttc(n)atctttaggg accttagatg(n)ctcctccag accagcttaa(n)caaggtaaga aaaaaaaga (n)caaaggaaa acaaaaaaga (n)caaaacacc
Contig length: Phrage values i Average error Fraction of Ph Number of cons Number of N's	Position 9347 10135 10135 10417 61959 61960 61961 61983 61983 61993 61993 62205 62205	90212 90216 90228 90236 90443 91405 122290

Distribution of Quality < 40 Bases

tgaagccact(n)gaaaagtaat

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PRI 01-JUN-2002
101834 TCCCCAAGACAATGGGGAAAATGTCTCCAAGGCATATCAGAGGTCTTCATGGCAGCCCAT 101893
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174874)
                                                                 101894 CCCATCACAGGCCCGGAGGCCTAGGAAAATGGTTTTGTAGGCCAGGCCCAGGAGCCCC 101953
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                                                                                                                                  101954 ATGCTGTGCGAGCCTAGGGACTTGGTGCCCTGTGTAACCAGCTGCTGGTGGTGGTGGCT
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complement(1624. .1682)
/rpt_family="MIR"
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/rpt_family="MER102"
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/rpt_family="AluY"
6571. .6616
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/db_xref="taxon:9606"
/chromosome="12"
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/rpt_family="L1ME3"
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                                                                                                                                                                                                                                                                                                            DB 9; Length 174874;
          Submitted (01-JUN-2002) DOE Joint Genome Institute, 28 Drive, Walnut Creek, CA 94598, USA Draft Sequence Produced by DOE Joint Genome Institute Profuced by DOE Joint Genome Institute Finishing Completed at Stanford Human Genome Center Www-shgc.stanford.edu at Stanford Goullty: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                            Pred. No. 4e-193;
0; Mismatches 175; Indels
                                                                                                                                                                                                                                                        52170 a 35353 c 35890 g 51461 t
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                              Score 689;
                                                                                                                                                                                                                                        /clone="RP11-213H15"
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80.18;
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmaliais Eutheria; Primates; Catarrhini; Hominidae; Homo.

Manmaliais Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18660)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Barbaria,J., Benteon,J., Binage,R., Biankenburg,K., Bonnin,D.,
Babork,J., Bowie,S., Briteva,M., Brown,E., Brown,M., Baryan,N.D.,
Babork,J., Bowie,S., Briteva,M., Brown,E., Brown,M., Baryan,N.D.,
Babork,J., Bowie,S., Briteva,M., Brown,E., Brown,M., Baryan,N.D.,
Babork,J., Bowie,S., Briteva,M., Chowdhry,I., Christopolos,C.,
Chen,G., Chen,Z., Chowdhry,I., Christopolos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davis,C., Davis,C., Davy-Carcoll,I., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Delaney,K.R., Delgado,O., Peng,A.L., Garcia,A., Hares,A., Hares,A., Harnandez,O., Hodgson,B., Jair,Y., Johlvet,S., Tuma,S., Jackbon,E., Marcia,A., Kalu,J., Kovah,C., Liu,J., Liu,A., Li,Z., Lichtarge,O., Liu,J., Lia,J., Lui,M., Loal,B., Marcia,M., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACO26107 186660 bp DNA linear HTG 06-FEB-2002 Homo sapiens chromosome 12 clone RP11-307L1, WORKING DRAFT SEQUENCE, 1 unordered piece.
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                                    55118 CCCGGATGTGAGACATGGAGTCAAAGGAGATCATTTTGGAGCTTTAAGATTTGACTGCCC 55177
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AAAATCCACAGACACTCAGTGCCAGCCTGTGAAAGCAGCAGGATGGAGTCTGTACCCTA 1154
                                                                                                                                     CAAAACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGA
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Homo sapiens.
Homo sapiens
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Chemistry: Dye-primer Bodipy: 82% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 186659 bases at least Q40
Consensus quality: 186660 bases at least Q30
Consensus quality: 186660 bases at least Q30
Estimated insert size: 187779; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 10.7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                      Department
                                                                                             Direct Submission
Submitted (19-MAR-2000) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 1, 2001 this sequence version replaced gi:13877175.
Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
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Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Direct Submission
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0; Mismatches 175; Indels
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Contact: hgsc-help@bcm.tmc.edu
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37346 c 35962 g 56263 t
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/db_xref="taxon:9606"
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1. .186660
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DNA linear HTG 24-AUG-2002
RP11-792C1 map 5, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1276 ACTGGATTTCGGACTTATATGGGCCCGTA-CCCCTTTGTTTTGGCCAATTTTTTCCATT 1334
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CAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAGAAGAAGTTGAGATTGAGGTTTGGGAA
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                                                                     CAAATCACTGGCCTGGAGGCCTAGGAAAATGGTTTTGTGGGACAGGCCCAGGGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTGCT
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Birren, B., Linton, L., Nusbaum, C. and Lander Homo sapiens chromosome 5, clone RP11-792C1 Unpublished
                                                                                                                                                                GTGCTGTGTGCAGCCTAGAGACTTGGTGCCCTGTGT-----
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Homo sapiens chromosome 5 clone
SEQUENCE, 36 unordered pieces.
AC044889
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
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NOTE: This is a 'working draft' sequence.
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouguslavkiy, L., Boukhaller, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Domlon, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graha, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Liue, S., Goyette, M., Grant, G., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., McCarthy, M., McEwan, P., McGurk, A., McGarnan, K., McPheeters, R., Meldrim, J., Mencus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T., Mihova, T., Miley, R., Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talanas, J., Tarsyers, M., Vale, K., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vorng, G., Zainoun, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W. J., Pierre, S., Narie, S., Sore, S., Sore, S., Wilson, B., Wu, X., Wyman, D., Verley, S., Narie, S., Sarker, S., Wyman, C., Wilson, B., Wu, X., Wyman, D., Verley, S., Sarker, Vo, A., Wilson, B., Wu, X., Wyman, D., Verley, S., Sarker, Vo, A., Wilson, B., Wu, X., Wyman, D., Verley, S., Sarker, S
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 189768)
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Insert size: 186258; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
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                          AUTHORS
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consists of 36 contign. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                            of 100 bp
contig of 1514 bp in length
of 100 bp
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contig of 1313 bp in length
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45266: contig of 4097 bp in length
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contig of 5620 bp in length
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67628: contig of 6546 bp in length
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72690: contig of 4962 bp in length
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79286: contig of 6496 bp in length
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92170: contig of 8619 bp in length
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
    86176 TGAAAGGGCCCAACATAGAGCTCGGGCTGTGGCTTCAGAAGGTGCAAGCCCCAAGCCTTG 86117
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Homo sapiens chromosome 5 clone RP11-54C4, complete sequence.
AC091982
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                                                                                                                                  Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced g1:14579765.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                 ACCTCCAATCAGATTTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTGC
                                                                                                                                                                              TGTAGGGGTGGGGTCCTCATGGAGAACCTCTGCAAGGGTAGTACAAAAGGGAAATGTTGG
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute.
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Pred. No. 4e-193;
0; Mismatches 175; Indels
123240 123339: gap of 100 bp
123340 137921: contig of 14582 bp in length
137922 138021: gap of 100 bp
138022 157913: contig of 19892 bp in length
157914 158013: gap of 100 bp
158014 189768: contig of 31755 bp in length.
                                                        Location/Qualifiers

1. 189768
                                                                                                                                                                                            /clone="RP11-792C1"
/clone_lib="RPCI-11 Human Male
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/note="assembly_fragment"
9795. .11004
/note="assembly_fragment"
11105. .12907
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/note="assembly_fragment"
3999. .5259
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17215. .18527
/note="assembly_fragment"
18628. .20561
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2385, .3898
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'note="assembly_fragment"
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13008. .14916
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15017. .17114
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                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                       Length 170368;
                                                                                                                                                                                                           Indels
            Sequence;
                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                          0; Mismatches 148;
                                                                                                                                                                                      Score 684.2; DB 9;
Pred. No. 1.1e-191;
      Quality: Phrap Quality >=40 99.8% of Sec Estimated Total Number of Errors is 0.2. STS Content: STGC-1085 G13672 SGC-53350 G36743 WI-14854 G22310 SGC-64132 G38710.
                                                                                                                                          /clone="RP11-54C4"
37145 c 34373 g 48826
                                                                                    Location/Qualifiers
1. .170368
/organism="Homo sapiens'
                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                 /chromosome="5"
www-shgc.stanford.edu
Quality: Phrap Quality
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82.08;
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Best Local Similarity 82.0°
Matches 827; Conservative
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Homo Sapiens chromosome 5 clone CTB-62P13, complete sequence.
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AC010312.5 GI:15281196
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Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 67984)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 23, 2001 this sequence version replaced 91:11079410. Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mit Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 67984)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                        24934 GTGTGACCTGCATATGAGACGTGGAGTCAAAAGAGATCATTTTGGATCTTTAAGACTTGA
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.1.
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81.9%; Pred. No. 1.5e-191;
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/chromosome="5"
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	Camarata, J., Campoptano, A., Chang, J. Collins, S., Collymore, A., Cooke, P., Diaz, J.S., Dodge, S., Faro, S., Ferre Galagan, J., Gardyna, S., Ginde, S., Grand-Pierre, N., Hagos, B., Heaford, Ilamazares, R., Landers, T., Lehoczky, MacLean, C., Macdonald, P., Marquis, N. McKernan, K., Morbeeters, Mihova, T., Menga, V., Morbeeters, Mihova, T., Menga, V., Murphy, T., Na Norman, C.H., O'Connor, T., O Donnell Peterson, K., Phunkhang, P., Pierre, N. P., P., P., P., P., P., P., P., P., P.	Rosetti, M., Roy, A., Santos, R., Schassery, P., Sougnez, C., Spencer, B., Straus, C., Spencer, B., Sudjanovic, N., Stravers, M., Travis, N., Viel, R., Vo.A., Wilson, B., Wu, X., Wilson, B.,	Kesearch, 310 Charles Street, Cambra 3 (bases 1 to 168502) Birren, B., Linton, L., Nusbaum, C., L. Anderson, S., Barna, N., Bastlen, V., Brown, A., Camarata, J., Campoplano, A. Choepel, Y., Colangelo, M., Collins, Scoke, P., DeArellano, K., Dewar, K., Ferreira, P., FitzHudh, W., Gage, D., Glande, S., Goyette, M., Grahlagos, B., Heaford, A., Horton, L., Hungos, B., Heaford, A., Horton, L., Hangos, B.,	Jones, C., Kamat, A., Karatas, A., Kel Lamazares, R., Landers, T., Lehoczky, MacLean, C., Macdonald, P., Major, J., McCarthy, M., McEwan, P., McKernan, K., Meneus, L., Mihova, T., Mlenga, V., Mu Norbu, C., Norman, C. H., O'Connor, T., Oliver, J., Peterson, K., Phunkhang, P Raymond, C., Retta, R., Rieback, M., R Seman, J., Rosetti, M., Roy, A., Santo Seaman, S., Severy, P., Spencer, B., S Strauss, N., Subramanian, A., Talamas	
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REPERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS AUTHORS		TITLE	REFERENCE AUTHORS		TITLE JOURNAL REFERENCE AUTHORS
CTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTCAGTTTCATAA  [	641 AGCAGTCCATCAAGACAAGGGGAAAATGTCTCCGGAGCATGTCAGAGGTCTTCAC 7358	AGCCTTGGCAGCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAGAAGTCAAGAATTGAGG			1208 GTCATGACCTGGACGTGGAGTCAAAGAGATCATTTGGAGCTTTAAGATTG 1267   111111   111111   111111   111111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   1111   1111   111

PRI 11-DEC-2001

linear

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168502 bp

AC091005

RESULT 13 AC091005/c LOCUS

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Nomo sepiens chromosome 15, clone RP11-1008C21, complete sequence. AC091005.9 GI:17488655
IISM homo saplens.
IIISM homo
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Direct Submission
Submitted (11-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 11, 2001 this sequence version replaced gi:15412474.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                ....- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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140. .191
//rpt_family="L2"
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complement(2627. .2637)
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/rpt_family="MIR"
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Center clone name: 1008_C_21
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/rpt_family="MLT2F"
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4319. .4348
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6377. .6382
/note="<30 qual SNGL region"
                                                                                                                                                                                     complement(10164. .10479)
/rpt_family="AluJo"
complement(11119. .11206)
/rpt_family="MIR"
13093. .13155
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/rpt_family="MER5A"
complement(19619. .20141)
/rpt_familv="ro"
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15738. .16076
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/rpt_family="MER5B"
complement(18937. .19116)
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complement(20145. .20670)
/rpt_family="MER69"
complement(20669. .21182)
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/rpt_family="MER69"
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8610. .8732
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                                .6621)
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18048. 18230
/rpt_family="MER5A"
18427. 18562
/rpt_family="MIR3"
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13446. .13751
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14102. .14669
/rpt_family="MLT1E2"
14671. .14973
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17512. .17576
/rpt_family="MLT1L"
17763. .17980
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                              complement(6414.
/rpt_family="MIR"
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complement(7718.
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complement(9591.
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                         45484 TCCCCAAGACAATGGGGAAAATGTCTCCAGGGCATGTCAGAGGTCTTCATAACAGCCCCT 45425
                                                                 45304 AAGGGGCCAACATAGAGCTCGGACTGTGGCTTCAGAGGGTGGAAGCCCCAAGCCTTGACA 45245
                                                                                                                                                                                                                                                                                 45184 TCCGCCTAGATTTTAGAAGATGTATAGAAACACCTGGATGCCCAGGCAGAAGTTTGCTGC 45125
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Homo sapiens BAC clone RP11-42414 from 2, complete sequence.
AC079614
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                                                                                                     GTGCTGTGTGCAGCCTAGAGACTTGGTGCCCTGTGTCCCCAGTTAATTCAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entire insert of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center, Washington
4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                               Submitted (04-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 5, 2001 this sequence version replaced g1:15209227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
2 (bases 1 to 131215)
Nguyen,C., Abbott,A. and Elliott,G.
The sequence of Homo sapiens BAC clone RP11-42414
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-SEP-2001) Genome University School of Medicine,
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Submitted (04-SEP-2000)
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4 (bases 1 to 131215)
Waterston, R.H.
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Waterston, R.H.
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Db 128525 GAGGTTTTCACAGCAGCCCTCCCATCACAGGCCTGGAGGCCTAGGAAAAACATGGTT 128584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 128645 CCCAGTCCACCGGTTGGTCGAAAGGGACCAAAAATATAGCTTCAGAGGGTGCAAACC 128704
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/rpt_family="(T)n"
23833. .24179
/note="match to EST AW023677 (NID:95877207) df58910.yl"
24692. .24726
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73390)

2 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonlin, D., Bouck, J., Buhage, K., Blankenburg, K., Bonlin, D., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazoss, S.K., Chacko, J., Chenge, C., Chen, R., Chau, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Dany, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elagy, N., Ford, J., Frantz, P., Gapisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Han, J., Hernandez, O., Harris, C., Harris, C., Hartis, C., Hartis, C., Hartis, C., Hodyan, Hodgson, A., Hodges, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hume, J., Ioshikhes, I., Jackson, L.E.,
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Homo sapiens 12 BAC RP11-547C5 (Roswell Park Cancer Institute Human
                          128705 TCAAGCCTTGGCAGCTTCCATGTGGTGTTGAGCCTGCAAGTGCCAGAACTCAAGAATTG 128764
                                                                                                                                128765 AGGTTTGGGAACCTCCCTGCCTAGATTTCAGAAGATATATGGAAACGCCTGGATGCCCAGGC 128824
                                                                                                                                                                                                                                   128945 TGAGAAGAGGCCACTGTCCTCCAGAACCCCAGAATGGTAGATCCACTGCCAGCTTGCACC 129004
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                                                                                                                                                                                                                                                                                                           GAAATGTTGGGTGGGAGCCCCCACACAGAGTCCCCAGTGGGGCTCCATCTAGTAGAGCTG 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1263 ATTTGACTGCCCCACTGGATTTCGGACTTATATGGGGCCCGT-ACCCCTTTGTTTGGCC
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Wheczyk, R., Wooden, S., Worley, K., Woo, C., Walliamson, A.,
Direct Submission
Alb. Upublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-007-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-JAN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Huguston, TX 77030, USA On Jan 1, 2001 this sequence version replaced gi:11138159.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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(bases 1 to 73390)
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Direct Submission
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COMMENT

gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

for and 2 in the standard of double strand coverage with a minimum of 2 ciones an reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality a region does not meet this standard, it will be indicated in th annotation as Low Coverage. completed to SEQUENCING READ COVERAGE: Sequencing is

OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

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351 GAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATAAGGAAGAAATTTCTAAGCAGCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCATTCAGTTTCATAAGGGAGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64695 AAGGGGCCAATGTAGAGCTCAGGCCATGGCTTCAGAGGGTGCAAGCTCCAAGCCTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTCCAAGTGGTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 GCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGATAAAAAAAGAAAAACCCATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 CAAATCACTGGCCTGGAGGCCTAGGAGAAAATGGTTTTGTGGGACAGGCCCAGGGTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 680; DB 9; Lk
80.2%; Pred. No. 1.8e-190;
live 0; Mismatches 175;
                                                                                                                   /rpt_family="L2"
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14261. .14435
/rpt_family="MIR"
14857. .13267
/rpt_family="MIR"
15776. .15819
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16714. .17041
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                                           complement(9689...9781)
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complement(9782..10068)
/rpt_family="AluSx"
complement(10069..11228)
                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="GA-rich"
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8972. .9004
/rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.2*
Matches 850; Conservative
                  repeat_region
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tcctgtggt(g)acaaagggtg
ccctgtggtg(a)caaagggtgt
ctgatcacag(c)actcctgagc
cactcctgag(c)taccttcat
tgaaattcac(a)cagaatcagg
                                                                                                                   4.24674e-07
0.000546837
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Phrap Value Range
                                                                                                                                                                                                           --- Consensus changing edits
Original+Context
tttgggcagg(n)acacaaatcc
                                                                                                                   Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Mumber of consensus changing edits:
Number of N's in consensus:
                                                                                                                                                                                                                                                                                                                                                            Distribution of Quality < 40
                                                                                                                                                                                                                                                       tccctgtggt(n)ncaaagggtg
ccctgtggtn(n)caaagggtg
ctgatcaag(n)actcctgagn
nactcctgag(n)taccttcat
tgaaattcac(n)cagaatcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(826...1067)
/rpt_family="MSTA"
complement(1070...2183)
/rpt_family="MSTA-internal"
complement(2211...2493)
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complement(2214...2875)
/rpt_family="MSTA-internal"
complement(2494...2875)
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complement(3718...2875)
                                                                         Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .73390
/organism="Homo sapiens"
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6930. .7009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5066. 5137
/rpt_family="MER5A"
complement(5082. 522
/rpt_family="MER5A"
5802. 6088
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/clone="RP11-547C5"
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/rpt_family="MIR"
                                                                                                     Phrap values in estimate:
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                             QUALSTAT-REPORT------
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Gaps

35;

Length 73390; Indels 64816

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1158 AACCGTAGTGGCAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGACCT 1217
                                                                                                      TGGATTTCGGACTTATATGGGGCCCGT-ACCCCTTTGTTTTGGCCCAATTTTTCCATTTG 1336
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